

From: Hutzell, Paula
Sent: Wednesday, January 02, 2002 4:16 PM
To: STIC-Biotech/ChemLib; Helmer, Georgia
Subject: FW: RUSH on FW: sequence search for 09/289346

approved

-----Original Message-----

From: Helmer, Georgia
Sent: Wednesday, January 02, 2002 4:08 PM
To: Hutzell, Paula
Subject: RUSH on FW: sequence search for 09/289346

Paula, I need this search as a Rush because it is due the next biweek. Thanks, Georgia

-----Original Message-----

From: Bui, Phuong
Sent: Wednesday, January 02, 2002 4:02 PM
To: Helmer, Georgia
Subject: RE: sequence search for 09/289346

It's fine. Send it to Paula as a RUSH.

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 1E01 TEL: 308-3534

12C14

-----Original Message-----

From: Helmer, Georgia
Sent: Wednesday, January 02, 2002 3:30 PM
To: Bui, Phuong
Subject: sequence search for 09/289346

[Bui, Phuong] Would **[Bui, Phuong]** you please do a search for the following sequences from application # 09/289346:

DNA encoding SEQ ID 2 - 10;
and polypeptides SEQ ID 2-10

Please do an interference search of DNA encoding SEQ ID 2 - 10
and polypeptides SEQ ID 2-10.

Thanks in advance,
Georgia L. Helmer Ph.D.
Patent Examiner
Crystal Mall 1, 9D14
AU 1638
703-308-7023
Georgia.Helmer@USPTO.gov

FOR OFFICIAL USE ONLY

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/3
Date Completed: 1/4
Searcher Prep/Review: 10
Clerical: 12
Online time: 10

TYPE OF SEARCH:
NA Sequences: 10
AA Sequences: 10
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: CS
WWW/Internet: CS
Other (specify): _____

Call 1-801-TELE-308-3334
Technical Info. Services
Toby Port
1-801-TELE-308-3334

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2002, 15:35:03 : Search time 144.17 Seconds
(without alignments)
35.965 Million cell updates/sec

Title: US-09-289-346a-2

Perfect score: 362

Sequence: 1 TLVWGEFVDGAAAGGQOT.....FQHNLNSLDRIFDKTEEP 70

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 52463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A: Geneseq_1101.*
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
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13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.*
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18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
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21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	362	100.0	70	21 AAB18678	Mutant peptide der
2	349	96.4	70	21 AAB18677	Peptide fragment f
3	349	96.4	356	21 AAB18687	Amino acid sequenc
4	341	94.2	70	21 AAB18685	Mutant peptide der
5	341	94.2	70	21 AAB18685	Mutant peptide der
6	337	93.1	70	21 AAB18693	Mutant peptide der
7	335	92.5	70	21 AAB18684	Mutant peptide der
8	335	92.5	70	21 AAB18690	Mutant peptide der
9	334	92.3	70	21 AAB18686	Mutant peptide der
10	333	92.0	70	21 AAB18689	Mutant peptide der
11	331	91.4	70	21 AAB18680	Mutant peptide der

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

12	331	91.4	70	21 AAB18691	Mutant peptide der
13	328	90.6	70	21 AAB18681	Mutant peptide der
14	327	90.3	70	21 AAB18683	Mutant peptide der
15	325	89.6	70	21 AAB18682	Mutant peptide der
16	325	89.6	70	21 AAB18679	Mutant peptide der
17	315	89.4	353	18 AAB34338	Bean golden mosaic
18	315	89.4	353	18 AAB34332	Bean golden mosaic
19	315	89.4	353	18 AAB34333	Bean golden mosaic
20	315	89.4	353	18 AAB34334	Bean golden mosaic
21	315	89.4	353	18 AAB34335	Bean golden mosaic
22	315	89.4	359	17 AAB48870	Sardinian tomato y
23	315	89.4	359	17 AAB48871	Sardinian tomato y
24	313	89.4	359	17 AAB48872	Sardinian tomato y
25	313	89.4	359	17 AAB70407	ORF 4 gene product
26	313	89.4	359	18 AAB34336	Tomato mottle viru
27	313	89.4	361	18 AAB34324	Tomato mottle viru
28	313	89.4	361	18 AAB34325	Tomato mottle viru
29	313	89.4	361	18 AAB34326	Tomato mottle viru
30	306.5	87.0	361	9 AAP70962	Product of ORF 4 f
31	306.5	87.0	361	9 AAP70963	Tobacco etch virus
32	300.1	85.2	357	18 AAB34329	Tomato yellow leaf
33	300	85.2	357	18 AAB34330	Tomato yellow leaf
34	300	85.2	357	18 AAB34331	Tomato yellow leaf
35	192	83.0	357	18 AAB34337	Tomato yellow leaf
36	69.5	19.2	512	19 AAB68473	HIV-1 strain YBF30
37	68.5	18.9	1693	21 AAB48457	Human laminin 5 po
38	68.5	18.9	1693	21 AAB48458	Human laminin 5 po
39	68.5	18.9	1713	21 AAB48459	Reduced sequence o
40	68.5	18.9	1713	21 AAB48458	Human laminin 5 po
41	68.5	18.9	1724	21 AAB48456	Human laminin 5 po
42	65.5	18.1	619	13 AAR27651	Human calcium chan
43	65.5	18.1	2161	14 AAR33545	Sequence of the al
44	65.5	18.1	2161	16 AAB71001	Human neuronal cal
45	65.5	18.1	2161	21 AAB10568	Human calcium chan

ALIGNMENTS

RESULT 1:
AAB18678
ID AAB18678 standard; peptide; 70 AA.
XX AAB18678;
XX AAB18678;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
DE Geminivirus: replication protein; Rep protein; AL1: transgenic plant;
DE ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
XX Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 12
XX Misc-difference 13 /note= "wild type residue replaced with Ala"
XX Misc-difference 15 /note= "wild type residue replaced with Ala"
XX Misc-difference 15 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.
XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.

(UYNC-) UNIV NORTH CAROLINA STATE.

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AII protein with a mutation in the Rb binding region
 FT
 XX
 XX
 XX
 XX Disclosure; Page 47-48; 73pp; English.
 CC The present sequence represents a geminivirus replication (Rep)
 CC protein, which is also known as AII. AII binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the AII protein are used
 CC to produce transgenic plants. The mutation in AII is present in a
 CC ribosome binding region, and expression of mutant AII protein imparts
 CC resistance to geminivirus infection in transgenic plants. Plants having the
 CC protein are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 XX Sequence 356 AA:

Query Match 96.4% Score 349; DB 21; Length 356;
 Best Local Similarity 95.7%; Pred. NO. 8.7e-35;
 Matches 67; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLWGEFVDCGAAAGCGCTSNDAARALNASSKEEALQITREKIPKYLQPHNLNSNL 60
 DB 110 TLWGEFVDCGAAAGCGCTSNDAARALNASSKEEALQITREKIPKYLQPHNLNSNL 169

OY 61 DRIFDKTPEP 70
 DB 170 drifdktp 179

RESULT 4
 AAB18685
 ID AAB18685 standard; peptide: 70 AA.
 XX
 XX AAB18685;
 XX
 XX
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AII) protein.

XX Geminivirus; replication protein; Rep protein; AII; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 XX Tomato golden mosaic virus.

FB Key Location/Qualifiers
 FT Misc-difference 10 /note= "wild type residue replaced with Ala"
 FT WT0200054573-AL.
 XX
 XX 21-SEP-2000.

PD 15-MAR-2000; 2000MO-US06759.

PF 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;

PI WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AII protein with a mutation in the Rb binding region
 FT
 XX
 XX
 XX
 XX Claim 53; Page 46; 73pp; English.
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AII. AII binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AII
 CC protein are used to produce transgenic plants. The mutation in AII is
 CC present in a ribosome binding region, and expression of mutant AII
 CC imparts resistance to geminivirus infection in transgenic plants. The
 CC plant is useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato leaf curl virus, tomato yellow leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, bean
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA:

Query Match 94.2% Score 341; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. NO. 1.1e-34;
 Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLWGEFVDCGAAAGCGCTSNDAARALNASSKEEALQITREKIPKYLQPHNLNSNL 60
 DB 1 TLWGEFVDCGAAAGCGCTSNDAARALNASSKEEALQITREKIPKYLQPHNLNSNL 60

OY 61 DRIFDKTPEP 70
 DB 61 drifdktp 70

RESULT 5
 AAB18688
 ID AAB18688 standard; peptide: 70 AA.
 XX
 XX AAB18688;
 XX
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AII) protein.

XX Geminivirus; replication protein; Rep protein; AII; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 XX Tomato golden mosaic virus.

FB Key Location/Qualifiers
 FT Misc-difference 19 /note= "wild type residue replaced with Ala"
 FT WT0200054573-AL.
 XX
 XX 21-SEP-2000.

PD 15-MAR-2000; 2000MO-US06759.

PF 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;

PI WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT
 XX
 PS Disclosure; Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC plant imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, cotton leaf curl virus, African cassava mosaic virus, Indian
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 93.48; Score 339; DB 21; Length 70;
 Best Local Similarity 92.98; Pred. No. 2.5e-34;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLVNGEFOVDDGAAAGCOTSDNAAAFALNASKEEAQLIIREKIPKYLQPHNLSNL 60
 DB 1 tlwgetqvdgrsarggcasdaaealnasskeeaqlirekipekylqghnlnsl 60
 QY 61 DRIFDKTPPEP 70
 DB 61 drifdktppep 70
 RESULT 6
 AAB18692
 ID AAB18692 standard; peptide: 70 AA.
 AC AAB18692;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 56 /note= "wild type residue replaced with Ala"
 FT Misc-difference 60 /note= "wild type residue replaced with Ala"
 FT
 XX WO2000054573-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 XX encoding a mutant A11 protein with a mutation in the Rb binding region
 PT
 XX
 PS Disclosure; Page 50; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC plant imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, cotton leaf curl virus, African cassava mosaic virus, Indian
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 SQ Sequence 70 AA;
 Query Match 93.18; Score 337; DB 21; Length 70;
 Best Local Similarity 92.98; Pred. No. 3.4e-34;
 Matches 65; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLVNGEFOVDDGAAAGCOTSDNAAAFALNASKEEAQLIIREKIPKYLQPHNLSNL 60
 DB 1 tlwgetqvdgrsarggcasdaaealnasskeeaqlirekipekylqghnlnsl 60
 QY 61 DRIFDKTPPEP 70
 DB 61 drifdktppep 70
 RESULT 7
 AAB18684
 ID AAB18684 standard; peptide: 70 AA.
 AC AAB18684;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 56 /note= "wild type residue replaced with Ala"
 FT Misc-difference 60 /note= "wild type residue replaced with Ala"
 FT
 XX WO2000054573-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.

15-MAR-2000; 2000NO-US06759.
18-MAR-1999; 99US-0125004.
09-APR-1999; 99US-0289346.
(UYNC-) UNIV NORTH CAROLINA STATE.
Hanley-Bowdoin L, Orozco BM, Kong L;
WPI; 2000-618851/59.
Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the RB binding region .
Claim 53; Page 46; 73pp; English.
The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyzes cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a ribosome binding region and expression of the mutant A11 protein imparts increased resistance to geminivirus infection. The plant, Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.
Sequence 70 AA:
Query Match 92.3%; Score 334; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. No. 7.9e-34;
Matches 65; Conservative 1; Mismatches 5; Indels 0;
QY 1 TLWGEFQVDGAAAGCQTSDNAAEALNASSKEALQIREKIPKYLFOFHNSNL 60
DB 1 TLWGEFQVDGAAAGCQTSDNAAEALNASSKEALQIREKIPKYLFOFHNSNL 60
QY 61 DRFDKTPPEP 70
DB 61 DRFDKTPPEP 70
RESULT 10
ID AAB18689 standard; peptide: 70 AA.
XX AAB18689;
XX AAB18689;
DT 22-JAN-2001 (first entry)
DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
DE Geminivirus; replication protein; Rep protein; A11; transgenic plant;
DE Ribosome binding region; resistance; geminivirus infection.
KW Synthetic.
OS QS
OS Tomato golden mosaic virus.
XX Key Location/Qualifiers
XX Misc-difference 22 /note= "wild type residue replaced with Ala"
FT FT Misc-difference 23 /note= "wild type residue replaced with Ala"
FT FT Misc-difference 24 /note= "wild type residue replaced with Ala"
FT FT W0200034573-A1.
XX XX

Job time: 153 sec

DT 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (Al1) protein.
 XX
 XX
 KW Geminivirus: replication protein; Rep protein; Al1; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 52 /note- "wild type residue replaced with Ala"
 FT Misc-difference 54 /note- "wild type residue replaced with Ala"
 FT Misc-difference 55 /note- "wild type residue replaced with Ala"
 FT Misc-difference 55 /note- "wild type residue replaced with Ala"
 XX W0200054573-Al.
 XX
 XX
 XX 21-SEP-2000.
 PD
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 PP
 XX 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 PR
 XX (UUNC-) UNIV NORTH CAROLINA STATE.
 PA
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 FT
 XX WPI: 2000-618851/59.
 DR
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 FT comprise a nucleic acid construct containing a nucleic acid sequence
 FT encoding a mutant Al1 protein with a mutation in the Rb binding region
 FT
 XX
 XX Claim 53: Page 44-45; 73pp: English.
 PS
 XX The present sequence represents a mutant peptide, derived from a
 XX geminivirus replication (Rep) protein, also known as Al1. Al1 binds
 XX DNA and interacts with other viral proteins. Mutants of Al1
 XX protein are used to produce transgenic plants. The mutation in Al1 is
 XX present in a ribosome binding region, and expression of mutant Al1 is
 XX protein imparts increased resistance to geminivirus infection in the
 XX plant. Mutant Al1 proteins are useful for producing plants having
 XX increased resistance or reduced sensitivity to a geminivirus such as
 XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 XX virus, bean dwarf mosaic virus, bean yellow mosaic virus, bean
 XX cassava mosaic virus, potato yellow mosaic virus, bean, golden mosaic
 XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 XX virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:

Query Match 89.8%; Score 325; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred No. 1e-32; 5; Indels 0; Gaps 0;
 Matches 64; Conservative 1; Mismatches 0; Gaps 0;

QY 1 TLWGEFQVDAAGGCGTSDNDAAEALNASSKEEAQLIREKIPKYLFOFHLNSNL 60
 ||||||||| : |||||||||||||||||||||||||||||||||||
 Db 1 tlwgefvgdrgsarggcqtsndaaeealnasskeeaqlirekipekylfaafalnsnl 60
 ||||||||| : |||||||||||||||||||||||||||||||||||
 OY 61 DRIRDKTEEP 70
 |||||||||
 Db 61 drifoktpep 70

Search completed: January 3, 2002, 15:37:36

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Run On: January 3, 2002, 15:35:04 ; Search time 72.79 Seconds
(without alignments)
73.255 Million cell updates

Sequence: 1 TLVWGEFQVDGAAAI

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 219241

Maximum DB seq length: 2000000000

Maximum Match 100%
Listing first 45 summaries

```
1: p1r1:*
```

4: pir4:*

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	349	96.4	352	1	QOCVLI			All protein - toma
2	249	68.8	361	1	QOCVPT			All protein - toma
3	236	65.2	358	2	S07594			hypothetical prote
4	232	61.3	352	2	S07594			hypothetical prote
5	222	61.3	352	2	S07594			hypothetical prote
6	218	60.2	349	2	Q32300			replicase - pepper
7	218	60.2	349	2	Q32300			replicase - pepper
8	215	59.4	359	2	S31875			All protein - pepp
9	212	58.6	355	2	S32593			hypothetical prote
10	212	58.6	355	1	QOCVMI			All protein - toma
11	209	57.7	358	2	S31870			All protein - toma
12	209	57.7	358	2	S31870			All protein - toma
13	209	57.7	385	2	S28360			All protein - beet
14	202	55.8	360	2	S55985			replication-associ
15	200	55.2	357	1	QOCVCI			All protein - toma
16	142	39.2	131	2	S45059			All protein (clone
17	124	34.3	347	1	QOCVSI			All protein - aqua
18	68.5	18.9	1713	2	S35347			adhesive ligand ep
19	65.5	18.1	1646	2	S35347			voltage-dependent
20	65.5	18.1	1646	2	JH0422			voltage-dependent
21	65.5	18.1	2161	2	JH0364			calcium channel a
22	65.5	18.1	2181	2	S43198			calcium channel a
23	65.5	18.1	2303	2	T42472			voltage-dependent
24	65	18.0	371	2	B69502			alcohol dehydrogen
25	64.5	17.8	299	2	B71967			probable peptidyl-
26	64.5	17.8	235	1	DBBS57			glycerolaldehyde-3-ph
27	64.5	17.8	235	1	DBBS57			phosphoglycerate-8
28	63.5	17.5	392	2	T45290			alcohol-CoA oxidase
29	63	17.4	397	2	B71078			probable NADH oxidase

Query Match 96.4% Score 349 DB 1: Length 352:

```

1 TLVWGEFQVDGAAAGCCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFQHNLSNL 60
|||||
111 TLVWGEFQVDGRSARGCQTSNDAAAEALNASSKEEALQIIREKIPKYLQFQHNLSNL 170
|||||

```

Qy 61 DRIFDKTPEP 70

䷀

Db 171 DRFDKTPEP 180

RESULT 2

QOCVPT

ALI protein - potato yellow mosaic virus (isolate venezuela)
C: species: potato yellow mosaic virus

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jun-2000

C;Accession: JU0364

K;Coutts, R.H.A.; Collin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72: 1515-1520, 1991

A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye

A;Reference number: JU0362; MUID:91311403

A;Accession: J00364
 X-Status: translation not shown

E; Status: translation not shown
 A; Molecule type: DNA

A; Residues: 1-361 <COU>

A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459

A: Map position: segment A

C; Superfamily: tomato golden mosaic virus AL1 protein

3

C-Date: 22-Nov-1993 sequence_revision 26-May-1995 text_change 20-Sep-1999
C-Accession: S31875
R:Torres-Pacheco, I.; Garzon-Tlizado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-Balboa, A.L. et al.: The complete nucleotide sequence of pepper huasteco virus and comparison submitted to the EMBL Data Library, February 1993

A:Description: Complete nucleotide sequence of pepper huasteco virus; Analysis and comparison of pepper huasteco virus sequences
A:Reference number: S31872
A:Accession: S31875
A:Species: Solanum glaucophyllum
A:Molecule type: DNA
A:Residues: 1-349 <TOR>
A:Cross-references: EMBL:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025
A>Note: the source is designated as pepper huasteco virus
C:Superfamily: tomato golden mosaic virus All protein

Query Match 60.2%; Score 218; DB 2; Length 349;
Pair Local Similarity 57.1%; Protein 14; Gaps 0;
Matches 40; Conservative 14; Mismatches 16; Indels 0;

QY 1 TLWKEFDVGGAAAGCGGOTSNDAAALNALNASKEEALQIIEKPEYLQFHHMNSNL 60
DB 1 :|||||: |||||: |::|||: |||||: |||||: |||||: |||||: |||||: |||||: ||
DB 110 TVPWGEFDIGDSARGCGQSANDTVAKLNASAEALQIIEKPQHFFLOFHNIYSNA 169

QY 61 DRIFDKTPPP 70
DB 170 NRIFTPTPP 179

RESULT 8
S32593 hypothetical protein C4 - tomato yellow leaf curl virus
C-Species: tomato yellow leaf curl virus
C-Date: 22-Nov-1993 sequence_revision 10-Nov-1995 text_change 20-Sep-1999
R:Khery-Pou, F.; Bendahmane, M.; Matzeil, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A>Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite virus
A:Reference number: S32588; MID:D92107660
A:Accession: S32593
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-353 <KH>
A:Cross-references: EMBL:X61153; NID:g62211; PIDN:CAA43466.1; PID:g62217
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C:Superfamily: tomato golden mosaic virus All protein

Query Match	59.4%	Score 215;	DB 2;	Length 359;
Best Local Similarity	55.18;	Prod. No. 5.7e-16;		
Matches	38;	Conservative 12;	Mismatches 19;	Indels 0;
Gaps	0;			
QY	2	LWGEFVQDQAAAGCCOTINDAAEALNASKKEALQITREKIPKYLQFQINLNSMLD 61		
		: : : : : : : : : :		
Db	111	LENGTFQIDGRSNGOOTINDAYAKIINAGSKOALGVRELAFDYVLYHFRINSMLD 170		
QY	62	RIFDQTPPEP 70		
		:::		
Db	171	KVFQVPPAP 179		
RESULT	9			
QJ02327				
Alt protein - Indian cassava mosaic virus				
N:Alternate names: replication-associated protein				
C:Date: 28-Aug-1985				
#sequence_revision 07-Oct-1994				
#text_change 20-Sep-1999				
C:Accession: J02327; S35893				
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.				
J. Gen. Virol. 74, 2437-2443, 1993				
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted cassava mosaic viruses in India				
J02326; M01D:34085670				
A: Molecule type: DNA				

A:Residues: 1-351 <HON>
A:Cross-references: EMBL: Z24756; NID: G935351; PIDN: CAA80891.1; PID: G584046
C:Superfamily: tomato golden mosaic virus All protein

Query Match 58.6% Score 212; DB 2; Length 351;
Best Local Similarity 55.7% Pred No. 1,26-15; Indels
Matches 40; Conservative 10; Mismatches 0; Gaps 0;

QY 4 WGEFVGGAAGAGCGTSSNDAAALNASSKEEAQIIIREKPKYLFQPHNLNSLDR1 63
Db 113 WGFQIDGSRAGGQGSANDAAALNASSGSKALKIIRLAPRIYDFPHHSSNDR1 172

QY 64 PDKTPEP 70
Db 173 FTKPEPP 179

RESULT 10
OOCVM1
All protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Accession: M146214
C:Title: Sequence revision 31-Mar-1992 *text_change 08-Apr-1994
C:Contig: 36214
C:Rischmuth, T.; Zilmatt, G.; Jeske, H.
C:Virology 178, 461-468, 1990
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as
A:Reference number: A36214; MUID: 91020984
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 358 <PR>
A:Cross-references: EMBL: X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus All protein

Query Match 58.6% Score 212; DB 1; Length 355;
Best Local Similarity 55.7% Pred No. 1,26-15; Indels
Matches 39; Conservative 13; Mismatches 18; Gaps 0;

QY 1 TLWKEFQVGGAAAGCGTSSNDAAALNASSKEEAQIIIREKPKYLFQPHNLNSL 60
Db 110 TAWSEFQIDGSRAGGQGTANDYAKALNAGDVQSNALILKEPQADYVQNHHSNLR 169

QY 61 DFRTKPEP 70
Db 170 ERTAKAPEP 179

RESULT 11
JQ1870
All protein - tomato mottle virus (isolate Florida)
C:Species: tomato mottle virus
C:Accession: JQ1870
C:Title: Sequence revision 17-Feb-1994 *text_change 07-May-1999
C:Abouzaid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated
A:Reference number: JQ1869; MUID: 93107858
A:Accession: JQ1870
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1358 <ABO>
A:Cross-references: GB: L14460
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus All protein

Query Match 57.7% Score 209; DB 1; Length 358;
Best Local Similarity 52.9% Pred No. 2,66-15; Indels
Matches 37; Conservative 17; Mismatches 16; Gaps 0;

```

QY 1 TLWGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 60
DB 107 TLWGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 166
QY 61 DRIFDKTPEP 70
DB 167 ERIFAKAPEP 176

RESULT 12
gene C1 protein - tomato yellow leaf curl virus
S39235
C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C:Accession: S39235
submitted to the EMBL Data Library, December 1995
A:Reference number: S39235
A:Accession: S39235
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <CRES>
A:Cross-references: EMBL:Z28390; NID:q1041671; PID:g1343964
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 57.7%; Score 209; DB 2; Length 359;
Best Local Similarity 53.6%; Pred. No. 2.6e-15;
Matches 37; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 61
DB 111 LWGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 170
QY 62 RIFDKTPEP 70
DB 171 KVFQPPAP 179

RESULT 13
S39360
ALL protein - beet curly top virus
C:Species: beet curly top virus
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
C:Accession: S28360
R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
EMBO J. 5, 1761-1767, 1986
A:Reference number: S28360
A:Accession: S28360
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <STA>
A:Cross-references: GB:M24597; EMBL:X04144; NID:g210878; PIDN:AAA42751.1; PID:g210679
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 57.7%; Score 209; DB 2; Length 385;
Best Local Similarity 52.9%; Pred. No. 2.8e-15;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 60
DB 137 TLWGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLD 196
QY 61 DRIFDKTPEP 70
DB 197 OKIFRPPDP 206

RESULT 14

```

```

S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 14-Jan-1998 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: S59885
R:Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A:Description: Nucleotide sequences from tomato leaf curl
d geminiviruses.
A:Reference number: S58346
A:Accession: S59885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <CHON>
A:Cross-references: EMBL:Z48182; NID:g944038; PIDN:CAA88229.1; PID:g974211
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 55.8%; Score 202; DB 2; Length 360;
Best Local Similarity 57.6%; Pred. No. 1.5e-14;
Matches 38; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 4 WGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLDRI 63
DB 113 FGVQIDGSRAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLDRI 172
QY 64 FDKTPEP 69
DB 173 FTSPEAE 178

RESULT 15
QOCVC1
ALL protein - tomato yellow leaf curl virus
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: U40779
R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a sin
A:Reference number: M40779; MFIID:92024070
A:Accession: U40779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <NAV>
A:Cross-references: GB:X15656; NID:g62204; PIDN:CAA33688.1; PID:g62207
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 55.2%; Score 200; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 2.5e-14;
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 4 WGEFQVDCGAAAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLDRI 63
DB 111 FGVQIDGSRAGCGCOTSDAAAEALNASSKEEALQIIREKIPEKYLQFHNLSNLDRI 170
QY 64 F 64
DB 171 F 171

Search completed: January 3, 2002, 15:40:08
Job time: 304 sec

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GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.
 OW protein - protein search, using sw model
 Run on: January 3, 2002, 15:38:54 ; Search time 43.68 Seconds
 (without alignments)
 58,758 Million cell updates/sec
 Title: US-09-289-346a-2
 Perfect score: 362
 Sequence: 1 TLVWGFQVDGAAAGGCGT.....POPHNLNLDRIFFKTPPEP 70

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 100059 seqs, 36664827 residues
 Total number of hits satisfying chosen parameters: 100059
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	96.4	332	1 VAL1-TGMV	P03567 tomato gold
2	236	85.5	338	1 VAL1-PYRV	P27436 potato yell
3	236	85.5	338	1 VAL1-CLVN	P14972 cassava lat
4	236	85.2	338	1 VAL1-TYIC	P36279 tomato yell
5	229	63.2	362	1 VAL1-TYIC	P36279 tomato yell
6	222	61.3	359	1 VAL1-TYIC	P36279 tomato yell
7	218	60.2	349	1 VAL1-PYRV	P02923 pepper huas
8	215	59.4	359	1 VAL1-TYIC	P27260 tomato yell
9	213	58.8	353	1 VAL1-BGMV	P05175 bean golden
10	213	58.8	353	1 VAL1-BGMV	P05175 bean golden
11	209	57.9	358	1 VAL1-ABMY	P11777 abutilon mo
12	209	57.2	361	1 VAL1-TMOV	P06557 tomato molt
13	200	55.2	357	1 VAL1-TYIC	P27259 tomato yell
14	124	34.3	347	1 VAL1-SLVC	P25048 squash leaf
15	68.5	18.9	1713	1 LMA3-HUMAN	P16787 homo sapien
16	65.5	18.1	1610	1 CCAD-MESAU	O95244 mesocricetu
17	65.5	18.1	1610	1 CCAD-HUMAN	Q01668 homo sapien
18	65.5	18.1	2298	1 YP75-RAJ1	P27732 rattus norv
19	65.5	17.8	339	1 YP75-RAJ1	P00162 bacillus st
20	64.5	17.8	339	1 G3P-BACST	P15115 bacillus co
21	64.5	17.8	335	1 G3P-BACCO	Q04791 anas platyr
22	64.5	17.8	335	1 SASE-ANAPL	P75465 mycoplasma
23	62.5	17.3	419	1 Y223-MYCN	P1617 tobacco yell
24	62	17.1	295	1 VAL1-TYDV	P12351 saccharomyc
25	62	17.1	1493	1 CYP1-YEAST	O62430 ctenorhabdi
26	60	16.6	397	1 YP75-RAJ1	P25075 drosophila
27	60	16.6	397	1 YP75-RAJ1	P25075 drosophila
28	60	16.6	447	1 CDS4-DRONE	P18080 gallus gall
29	60	16.6	513	1 HEMO-CHICK	P37893 caulobacter
30	59.5	16.4	863	1 AMPN-CAUCR	P51339 porphyra pu
31	59	16.3	129	1 RK12-PORPU	P25349 saccharomyc
32	59	16.3	247	1 YCP4-YEAST	P56112 helicobacte
33	58.5	16.2	295	1 Y175-HELPS	

RESULT 1

VAL1-TGMV 1
 ID VAL1-TGMV STANDARD; PRT; 352 AA.
 AC P03567;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE AL1 PROTEIN.
 DE AL1.
 OS Tomato golden mosaic virus (TGMV).
 GN Tomato golden mosaic virus.
 OC Virginales; Tombivirales; Geminiviridae; Begomovirus.
 NC NCBI_TaxID=10831;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
 RT *Complete nucleotide sequence of the infectious cloned DNA components
 of tomato golden mosaic virus: potential coding regions and regulatory
 elements.
 RT EMBL J 3:2197-2205(1984).
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 CC EMBL: K02029; -: NOT ANNOTATED.CDS.
 DR PIR: A04170; QQCVL1.
 DR InterPro: IPR001191; Geminin_AL1.
 DR Pfam: PF00799; Geminin_AL1; 1.
 DR PRINTS: PR00228; GEMININ_AL1.
 DR PROSITE: PS000736; Geminin_AL1; 1.
 DR ATP-binding.
 KW ATP-BINDING.
 FT FT_BIND 223 230 ATP (POTENTIAL).
 SQ SEQUENCE 352 AA: 40332 MW: 3339318P5644B4A4 CRC64;

Best Match
 Query Local Similarity 95.48; Score 349; DB 1; Length 352;
 Mismatches 67; Conservative 1; Mismatches 0; Gaps 0;
 OY 1 TLVWGFQVDGAAAGGCGTSDNAAAEALNASSKEALQIRKIPKLYFQPHNLNLSL 60
 DB 111 TLVWGFQVDGAAAGGCGTSDNAAAEALNASSKEALQIRKIPKLYFQPHNLNLSL 170

RESULT 2

VAL1-PYRV 2

```

ID VALL_PYAWV STANDARD: PRT: 361 AA.
AC P27258:
AC 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
CC AL1 PROTEIN: new mosaic virus (isolate Venezuela).
CC AL1 PROTEIN: ssDNA viruses: Geminiviridae; Begomovirus.
CC NCBI_TaxID=10826;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.:
RA The nucleotide sequence of the infectious cloned DNA components of
RA the tobacco etch virus.
RL J. Gen. Virol. 72:1515-1520(1991).
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CC
CC EMBL: D00940; BAA0782.1;
CC PIR: J00364; QCCVPT; Gemin1-ALL1.
CC Pfam: PF00799; Gemin1-ALL1.
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00228; GEMCOATCLVLL.
CC Problem: PD000736; Gemin1-ALL1; 1.
CC ATP-binding: 222 229 ATP (POTENTIAL).
CC NP_BIND 361 AA; 40650 MW; 562435BF1264393 CRC64;
CC FT
CC SQ
Query Match 68.8%; Score 249; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 4.5e-20;
Matches 46; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
Oy 1 TLWGEPQVQGAAGCGTSDNDAAEALNASKEPAQLQIREKIPKYLQFHNLSNL 60
Db 110 TTEGLFQIDRSARGSQQTNDAAEALNASKEPAQLQIREKIPKYLQFHNLSNL 169
Oy 61 DRIFDKTPE 69
Db 170 DRIFMAPE 178
Query Match 65.2%; Score 236; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-18;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
Oy 1 TLWGEPQVQGAAGCGTSDNDAAEALNASKEPAQLQIREKIPKYLQFHNLSNL 60
Db 109 TVENGQFQIDRSARGSQQTNDAAEALNASKEPAQLQIREKIPKYLQFHNLSNL 168
Oy 61 DRIFDKTPE 70
Db 169 DRIFQPPAP 178

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RESULT 4
VALL_CLVKN STANDARD: PRT: 358 AA.
ID VALL_CLVKN STANDARD: PRT: 358 AA.
AC P14972:
AC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
CC AL1 PROTEIN (40.4 KDa PROTEIN).
CC AC1.
CC OS Cassava latent virus (strain Nigerian).
CC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
CC NCBI_TaxID=10819;
RN [1]
RN SEQUENCE FROM N.A.
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.:
RA "Nucleotide sequence of the infectious cloned DNA components of
RA African cassava mosaic virus (Nigerian strain).";
RL Nucleic Acids Res. 18:197-198(1990).
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CC
CC EMBL: X17095; GAA34553.1;
CC PIR: S07594; S07594.
CC InterPro: IPR001191; Gemin1-ALL1.
CC Pfam: PF00799; Gemin1-ALL1; 1.
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00228; GEMCOATCLVLL.
CC Problem: PD000736; Gemin1-ALL1; 1.
CC ATP-binding: 220 227 ATP (POTENTIAL).
CC NP_BIND 358 AA; 40435 MW; 1DB16B0CB2D5E2C CRC64;
CC FT
CC SQ
Query Match 65.2%; Score 236; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 1.2e-18;
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

```



```

Oy 1 TLVWGFEVDGAAAGCGCOTSDAAAFALMASSEKPALOITREKIPKYLQFPHNLNSML 60
Db 109 TVWGQFQIDGARSAGCGQSDNDAAAFALMASSEKPALOITREKIPKYLQFPHNLNSML 168
Oy 61 DRIFDKTPPE 70
Db 169 DRIFDQFPAP 178

RESULT 5
VALL_TYLCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
CW
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxId=36447;
RX MEDLINE=93139778; PubMed=9423446;
RX RY J.B. Rigidon J.B., Krake C.R., Mullineaux P.M., Rezaiian M.A.:
RT "Genomic organization and genome organization of tomato leaf curl
RL -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
J. Gen. Virol. 74:147-151(1993).
DR PIR: JQ1887; JQ1887.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCORTALL.
DR PRODOM: PR000736; GEMCORTALL.
DR ATP-Binding. 221 228 ATP (POTENTIAL).
KW ATP-Binding, 221 228 ATP (POTENTIAL).
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B704098 CRC64;
[1]

Query Match 63.3%; Score 229; DB 1; Length 362;
Best Local Similarity 53.3%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 14; Indels 16; Gaps 1;

Oy 1 TLVWGFEVDGAAAGCGCOTSDAAAFALMASSEKPALOITREKIPKYLQFPHNLNSML 60
Db 110 TLWGFEQIDGARSAGCGQSDNDAAAFALMASSEKPALOITREKIPKYLQFPHNLNSML 169
Oy 61 DRI-----EKTPE 69
Db 170 DRIFTPLEVYVPSLSSDFRYPE 194

RESULT 6
VALL_TYLCU STANDARD; PRT; 359 AA.
ID VALL_TYLCU
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
CW
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxId=57139;
RX MEDLINE=94256836; PubMed=8138442;
RX Morris E., Hidalgo E., Accotto G., Moriones E.:
RT "High similarity among the tomato yellow leaf curl virus isolates
RT Infectious clone from Spain.";
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Arch. Virol. 135:165-170(1994).
-1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL: Z25751; CAA81026.1;
DR PIR: S39211; S39211.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCORTALL.
DR PRODOM: PR000736; GEMCORTALL.
DR ATP-Binding. 221 228 ATP (POTENTIAL).
KW ATP-Binding, 221 228 ATP (POTENTIAL).
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41065 MW; 2D170A51EF8DA3EC CRC64;

Query Match 51.3%; Score 222; DB 1; Length 359;
Best Local Similarity 58.0%; Pred. No. 4.2e-17;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGFEVDGAAAGCGCOTSDAAAFALMASSEKPALOITREKIPKYLQFPHNLNSML 61
Db 111 LEMGTFOIDGARSAGCGQSDNDAAAFALMASSEKPALOITREKIPKYLQFPHNLNSML 170
Oy 62 RIFDKTPPE 70
Db 171 RVFQVPPAP 179

RESULT 7
VALL_PHUV STANDARD; PRT; 349 AA.
ID VALL_PHUV
AC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALL PROTEIN.
CW
OS Pepper huasteco virus (PHV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxId=28349;
RX MEDLINE=94013007; PubMed=8409944;
RX Rivera-Bustamante R.F., Gordon-Tiznado J.A., Herrera-Estrella L.,
FA "Complete nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses.*;
RL J. Gen. Virol. 74:2225-2231(1993).
-1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL: X70418; CAA49356.1;
DR PIR: S31875; S31875.
DR InterPro: IPR001191; Geminl_AL1.
DR Pfam: PF00799; Geminl_AL1; 1.
DR PRINTS: PR00227; GEMCORTALL.
DR
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DR ProDom: PD000736; Gemini_AL1: 1.
KW ATP-binding. 221 228 ATP (BY SIMILARITY).
FT NP_BIND 349 AA: 39722 MW: DSPAE76CD56370F4 CRC64:
SQ SEQUENCE 349 AA: 39722 MW: DSPAE76CD56370F4 CRC64:

Query Match 60.28; Score 218; DB 1; Length 349;
Best Local Similarity 57.18; Pred. No. 1.1e-16; Indels 0; Gaps 0;
Matches 40; Conservative 14; Mismatches 16;

OY 1 TLWGEFVQDGAAGGCGTSDNDAEALNASKEEALQIIREKIPKYLQFHNLNSL 60
DB 110 TLWGEFVQDGAAGGCGTSDNDAEALNASKEEALQIIREKIPKYLQFHNLNSL 169
OY 61 DRIFDKTPPEP 70
DB 170 NRIFQTPPEP 179

RESULT 9
ID VALL_BGMV STANDARD: PRT: 353 AA.
AC POS175: 1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DF AL1 PROTEIN (40.2 KDA PROTEIN).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OY NCBI_TaxID=10833;
DB SEQUENCE FROM N.A.
RX Howarth A.J., Caton J., Bossert M., Goodman R.M.;
RA "Nucleotide sequence of bean golden mosaic virus and a model for gene
RT regulation in geminiviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC -----
DR EMBL: M10070; AAA6318.1;
RX InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1: 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Gemini_AL1: 1.
DR NCBI_TaxID=10833;
FT NP_BIND 169-222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA: 40190 MW: 80FA779DF6029A34 CRC64:

Query Match 58.88; Score 213; DB 1; Length 353;
Best Local Similarity 57.18; Pred. No. 4e-16; Indels 0; Gaps 0;
Matches 40; Conservative 14; Mismatches 16;

OY 1 TLWGEFVQDGAAGGCGTSDNDAEALNASKEEALQIIREKIPKYLQFHNLNSL 60
DB 110 TLWGEFVQDGAAGGCGTSDNDAEALNASKEEALQIIREKIPKYLQFHNLNSL 169
OY 61 DRIFDKTPPEP 70
DB 170 NRIFQTPPEP 179

RESULT 10
ID VALL_ABWV STANDARD: PRT: 355 AA.
AC P21947:
DT 01-AUG-1991 (Rel. 19, Created)
DE 01-AUG-1991 (Rel. 19, Last sequence update)
DF AL1 PROTEIN.
GN AC1.
OS Abutilon mosaic virus (isolate West India).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OY NCBI_TaxID=10816;
DB SEQUENCE FROM N.A.
RX Frischmuth T., Zimmatt G., Jaske H.;
RA "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features.";
RL Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

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CC -----
DR EMBL: X15993; -- NOT_ANNOTATED_CDS.
DR PIR: A2471;
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR ProDom: PD000736; Gemini_AL1.1.
KW ATP-binding. 221 228 ATP (POTENTIAL).
FT NP_BIND 222 229
SQ SEQUENCE 355 AA; 40257 MW; 16ACAA863251E95 CRC64;
Query Match 58.6%; Score 212; DB 1; Length 355;
Best Local Similarity 55.7%; Pred. No. 5.1e-16;
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
OY 1 TLVGFQVDCAAAGCCTSDNDAARFALMASKEKALQIIRKIPKYLQFHNLSNL 60
DB 110 TAEGRFQIDGRSANGCOQTANDSYAKALNAGVQSALNILEKQPKDFVLOHNNLSNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179
RESULT 11
VALL_BCTV
ID VALL_BCTV STANDARD; PRT: 358 AA.
AC P14991;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
OS Bacteriophage phi801 (BCTV).
OS Best curly tail virus (BCTV).
OC Viruses; ssDNA viruses; Geminiviridae; Curtovirus.
OX NCBI_TaxID=10840;
RN [1]
RP Stanley J., Markham P.G., Callis R.J., Pinner M.S.:
RA The nucleotide sequence of an infectious clone of the geminivirus
RT BCTV. Nucleic Acids Res. 19: 1761-1767 (1991).
RL EMBL J.5:1761-1767 (1991).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL: X04144; -- NOT_ANNOTATED_CDS.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR ProDom: PD000736; Gemini_AL1.1.
KW ATP-binding. 222 229 ATP (POTENTIAL).
FT NP_BIND 222 229
SQ SEQUENCE 358 AA; 40889 MW; 39A45FE3C0B9C33 CRC64;
Query Match 57.7%; Score 209; DB 1; Length 358;

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Best Local Similarity 52.9%; Pred. No. 1.1e-15;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
OY 1 TLVGFQVDCAAAGCCTSDNDAARFALMASKEKALQIIRKIPKYLQFHNLSNL 60
DB 110 TAEGRFQIDGRSANGCOQTANDSYAKALNAGVQSALNILEKQPKDFVLOHNNLSNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179
RESULT 12
VALL_TMOV
ID VALL_TMOV STANDARD; PRT: 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
OS Tomato mottle virus (TMOV).
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP SEQUENC FROM N.A. PubMed=1469361.
RA SEDLINGER, M. Polak, J.F. Hiebert G.:
RA "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229 (1992).
CC -/- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC -----
DR EMBL: U11460; X852414.1;
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR ProDom: PD000736; Gemini_AL1.1.
KW ATP-binding. 222 228 ATP (BY SIMILARITY).
FT NP_BIND 222 228
SQ SEQUENCE 361 AA; 40516 MW; 813865CEAC0950 CRC64;
Query Match 57.7%; Score 209; DB 1; Length 361;
Best Local Similarity 52.9%; Pred. No. 1.1e-15;
Matches 37; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
OY 1 TLVGFQVDCAAAGCCTSDNDAARFALMASKEKALQIIRKIPKYLQFHNLSNL 60
DB 110 TAEGRFQIDGRSANGCOQTANDSYAKALNAGVQSALNILEKQPKDFVLOHNNLSNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179
RESULT 13
VALL_TYLCV
ID VALL_TYLCV STANDARD; PRT: 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE GN ALL PROTEIN (C1 PROTEIN).
OC Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10837;
RA RA
RP SEQUENCE FROM N.A.
RA MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeldan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 185:151-161(1991).
RL -----
RL 1. SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC -----
CC DB EMBL: X15656; CA33688.1;
CC PIR: D40779; QOCVCL.
CC InterPro: IPR001191; GeminI_AL1.
CC Pfam: PF00799; GeminI_AL1.
CC PRINTS: PR00227; GEMCOATAL1.
CC PROSITE: PS00228; GEMCOATCIVL1.
CC ATP-binding; GeminI_AL1; 1.
KW NP_BIND 219 226 ATP (POTENTIAL).
FT SEQUENCE 357 AA; 40678 MW; 939AB68E1AB3B2A7 CRC64;
SQ
Query Match 55.2%; Score 200; DB 1; Length 357;
Best Local Similarity 62.3%; Pred. No. 1.1e-14;
Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
OY 4 WGFVDGAAAGGCGTSDNAAALNMASSKEAQLIIRKTPKYLQPHNLNSLDRI 63
DB 111 FGVSDIGRSARGGQGGANDAYAPALNMGSKSEALNLRKPKDYTLQPHNLNSLDRI 170
OY 64 F 64
DB 171 F 171
RESULT 14
ID VAIL_SLCV STANDARD; PRT; 347 AA.
OC 72048; 1992 (Rel. 24, Created)
OC 01-DEC-1992 (Rel. 24, Last annotation update)
OC 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALL PROTEIN.
OC Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10829;
RA RA
RP SEQUENCE FROM N.A.
RA MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdus I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 180:59-69(1991).
RL -----
RL 1. SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC -----
CC DB EMBL: M38183; AAC32410.1; AUT_INIT.
CC PIR: C36785; QOCVSI.
CC InterPro: IPR001191; GeminI_AL1.
CC PRINTS: PR00227; GEMCOATAL1.
CC PROSITE: PS00228; GEMCOATCIVL1.
CC ATP-binding; GeminI_AL1; 1.
KW NP_BIND 218 225 ATP (POTENTIAL).
FT SEQUENCE 347 AA; 39110 MW; AFDABDDDE122110E CRC64;
SQ
Query Match 34.3%; Score 124; DB 1; Length 347;
Best Local Similarity 37.9%; Pred. No. 2.2e-06;
Matches 25; Conservative 14; Mismatches 23; Indels 4; Gaps 1;
OY 5 GFEVDGAAAGGCGTSDNAAALNMASSKEAQLIIRKTPKYLQPHNLNSLDRI 64
DB 116 QYKVSQ ---GSKNDQYHNYNRGAGNDIIRAGDPTFYVHNLNANVLP 171
OY 65 DKTPPE 70
DB 172 QKPPPE 177
RESULT 15
ID LMA3_HUMAN STANDARD; PRT; 1713 AA.
OC Q16787; Q13679; Q13680;
OC 01-NOV-1997 (Rel. 35, Created)
OC 01-NOV-1997 (Rel. 35, Last sequence update)
OC 20-AUG-2001 (Rel. 40, Last annotation update)
DE LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KDA SUBUNIT) (E170).
OC LMA3;
OC Hs; H sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=keratinocytes;
OC Medline=9429426; PubMed=8077230;
OC McFiz G., Vandevert D.R., Carter W.C.;
RT "Cloning of the Lma3 gene encoding the alpha 3 chain of the adhesive
RT ligand epiligrin. Expression in wound repair.";
RL J. Biol. Chem. 269:22779-22787(1994).
RN [2]
RP MEDLINE=96163880; PubMed=8586427; Galliano M.-F., Cristiano A.M.,
OC Uitto J., Brodian S., Pineschi G., Pineschi G.;
RT "Cloning of the lamin alpha 3 chain gene (LMA3) and identification
RT of a homozygous deletion in a patient with Herlitz functional
RT epidermolysis bullosa.";
OC Genomics 30:273-280(1995).
RN [3]
RP FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
OC RECEPTOR. IS THOUGHT TO BE INVOLVED IN CELL ADHESION AND ORGANIZATION OF
OC CELL TO EXTRACELLULAR MATRIX COMPONENTS. INTERACTS WITH OTHER
OC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC
CC 1-1- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
CC 6/BETA-4 IN HEMIDESMOSOMES. (2) SIGNAL TRANSDUCTION VIA TYROSINE
CC PHOSPHORYLATION OF PP125-FAK AND P80. (3) DIFFERENTIATION OF
CC KERATINOCYTES.
CC LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLYCOLES AT EACH END.
CC THE ALPHA-3 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILIGRIN/LAMININ/
CC NECTIN), AND POSSIBLY ALSO A COMPONENT OF LAMININ-6 (K-LAMININ)
CC

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FT DOMAIN 1686 1713 COILED COIL (POTENTIAL).
FT DISULFID 67 76 BY SIMILARITY.
FT FT DISULFID 69 83 BY SIMILARITY.
FT FT DISULFID 86 95 BY SIMILARITY.
FT FT DISULFID 98 111 BY SIMILARITY.
FT FT DISULFID 114 126 BY SIMILARITY.
FT FT DISULFID 129 140 BY SIMILARITY.
FT FT DISULFID 147 166 BY SIMILARITY.
FT FT DISULFID 171 184 BY SIMILARITY.
FT FT DISULFID 202 202 INTERCHAIN (PROBABLE).
FT FT DISULFID 205 205 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 658 660 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 542 542 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 645 645 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 682 682 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 882 882 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 964 964 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 1108 1108 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 1131 1131 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 1325 1325 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 1477 1477 N-LINKED (GLCNAC..-) (POTENTIAL).
FT CARBOHYD 1567 1567 N-LINKED (GLCNAC..-) (POTENTIAL).
FT VAMPPLIC 1 45 N-LINKED (GLCNAC..SSQAKSLGCDMLQASVVE)
PEPS -> KYSSGVGYLTQKSAFLGDWYELKSPDVL
TQIMSLIVETNPTREDFLRHGRVHVINEINRHAASSRPV
SGSRIALAVELCAFCAPAYAGDSC (IN ISOFORM B).
W -> R (IN REF. 2).
ATG -> GNC (IN REF. 2).
M -> K (IN REF. 2).
C -> S (IN REF. 2).
E -> D (IN REF. 2).
D -> A (IN REF. 2).
G -> A (IN REF. 2).
Query Match 18.9%; Score 68.5; DB 1: Length 1713;
Ref. Local Similarity 35.1%; Ref. Num 15;
Matches 22/ Conservative 11; Mismatches 21; Indels 7; Gaps 3;
QY 9 VDGAAGAAGCGTCNDAAAEALN--ASSEKAQL-IREKIPEXYLFQFHNLNSLDRIFD 65
| | | : | | | : | | | : | | | : | | | :
DB 553 VDAATAYENILNAIKAADRAANRASASALQTIVREDLPK---AKTLSSNSDKLN 608
QY 66 K 66
DB 609 E 609
Search completed: January 3, 2002, 15:57:14
Job time: 1100 sec

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SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
1	298	82.3	352	12	Q9P000	Q9E000 tomato rugo
2	281	77.6	226	12	Q9Y727	Q9Y727 leonurus mo
3	281	77.6	226	12	Q9WHF6	Q9WHF6 tomato mild
4	279	77.1	361	12	Q67574	Q67574 bean golden
5	277	76.5	225	12	Q9D0R1	Q9D0R1 cowpea gold
6	277	76.5	314	12	Q9E1R8	Q9E1R8 sweet potato
7	274	76.7	185	12	Q9E1R8	Q9E1R8 sweet potato
8	274	76.7	185	12	Q9E693	Q9E693 sweet potato
9	266	73.5	149	12	P48975	P48975 macroptiliu
10	266	73.5	233	12	Q9YL44	Q9YL44 macroptiliu
11	260	71.8	234	12	Q93180	Q93180 potato yell
12	257	71.0	190	12	Q9Z089	Q9Z089 tobacco lea
13	257	71.0	190	12	Q9Z084	Q9Z084 tobacco lea
14	256	70.7	190	12	Q9M427	Q9M427 tobacco lea
15	256	70.7	208	12	Q9Z0C4	Q9Z0C4 tobacco lea
16	254	70.2	208	12	Q9Z0C8	Q9Z0C8 tobacco lea
17	254	70.2	208	12	Q9Z0B8	Q9Z0B8 tobacco lea
18	252	69.6	208	12	Q9Z0B6	Q9Z0B6 tobacco lea
19	251	69.3	203	12	Q9Z0B3	Q9Z0B3 tobacco lea

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009727
ID Q09727 PRELIMINARY; PRT: 226 AA.
AC Q1-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE REP.
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=58177;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=LEWY-BRAZIL 1;
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U92532; AAB51157.1; -
DR InterPro: IP001191; GeminI_AL1.
DR Pfam: PF00799; GeminI_AL1; 1.
DR PRINTS: PD00273; GEMCOATALL.
DR PRODOM: PD000736; GeminI_AL1.
FT NON_TER 226 AA; 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6E766083FC5 CRC64;

Query Match 77.6%; Score 281; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 9.2e-23;
Matches 54; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLVGEFQVDCGAAGCGTSDNDAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 60
DB 111 TVMGFEQVDCGARGGQGTANDAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 170
QY 61 DRFDKTPPEP 70
DB 171 DRFAKAPPEP 180

RESULT 3
ID Q9WHF6 PRELIMINARY; PRT: 226 AA.
AC Q1-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
OS tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
OX NCBI_TaxID=52543;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=BN96-HSKW;
RA Nakhlia M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M., Maxwell D.P.;
RL "Molecular characterization and DNA-based detection methods for vegetable-infecting geminiviruses in Central America.";
DR EMBL: AF131071; A033471.1; EMBL/GenBank/DBJ databases.
DR InterPro: IP001191; GeminI_AL1.
DR Pfam: PF00799; GeminI_AL1; 1.
DR PRODOM: PD00273; GEMCOATALL.
DR NON_TER 226 AA; 226
SQ SEQUENCE 226 AA; 25941 MW; 2E41167112871A23 CRC64;

Query Match 77.6%; Score 281; DB 12; Length 226;
Best Local Similarity 77.9%; Pred. No. 9.2e-23;
Matches 51; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLVGEFQVDCGAAGCGTSDNDAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 60
DB 111 TVMGFEQVDCGARGGQGTANDAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 170
QY 61 DRFDKTPPEP 70
DB 171 DRFAKAPPEP 180

RESULT 4
ID Q67574 PRELIMINARY; PRT: 361 AA.
AC Q1-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1999 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G., Maxwell D.P., Russell D.R.;
RL Phytopathology 81:980-985(1991).
RN [2] SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C., Morales F.J.; Maxwell D.P.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M88686; AAA46312.1; -
DR InterPro: IP001191; GeminI_AL1.
DR Pfam: PF00799; GeminI_AL1; 1.
DR PRINTS: PD00273; GEMCOATALL.
DR PRODOM: PD000736; GeminI_AL1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.1%; Score 279; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 2.6e-22;
Matches 51; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 WSEFQVDCGAAGCGTSDNDAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 63
DB 113 WGFQVDCGARGGQGTANDAAEALNASSKEEALQIREKIPKYLQFPHNLNSL 172
QY 64 DRFDKTPPEP 70
DB 173 DRFAKAPPEP 179

RESULT 5
ID Q9QDB1 PRELIMINARY; PRT: 225 AA.
AC Q1-NOV-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
OS cowpea golden mosaic geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=CGNV-BR;
RA Faria J.C.;
RL "Partial nucleotide sequence of cowpea golden mosaic geminivirus from Brazil.";
SQ Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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ID P88975; PRELIMINARY; PRT: 149 AA.
 AC DB 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DE 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 GN REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 DR ACL.
 DB 110 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 169
 QY 1 TLWGEFQVQGAAGCGCOTSDNAAEALNSGTEKALQIIRKIPKYLPOFHNLNSL 60
 DB 110 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 169
 QY 61 DRIFDKTPEP 70
 DB 170 DRIFDKMDEP 179
 NCBI_TaxID=51676;
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RC ROYCE M.E.;
 RL Thesis (1996). Biochemistry, University of the West Indies, Jamaica.
 RL EMBL: U75278; AAR36919.1; -
 DR InterPro: IPR001191; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1; 1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR ProDom: PD000736; Gemin1_AL1; 1.
 DR ProDom: PD000736; Gemin1_AL1; 1.
 FT NON_TER 149 149
 SQ SEQUENCE 149 AA: 16785 MW: 84CF5RED4C9CD508 CRC64;

Query Match 73.5%; Score 266; DB 12: Length 149;
 Best Local Similarity 68.6%; Pred. No. 2.4e-21;
 Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLWGEFQVQGAAGCGCOTSDNAAEALNSGTEKALQIIRKIPKYLPOFHNLNSL 60
 DB 52 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 111

QY 61 DRIFDKTPEP 70
 DB 112 DRIFDKMDEP 121

RESULT 10
 ID Q9YL44 PRELIMINARY; PRT: 233 AA.
 AC DB 09YL44; 999 (Tremblrel. 10, Created)
 DT 01-MAY-1997 (Tremblrel. 10, Last sequence update)
 DE 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 GN REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 DR REP.
 DB 110 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 169
 QY 1 TLWGEFQVQGAAGCGCOTSDNAAEALNSGTEKALQIIRKIPKYLPOFHNLNSL 60
 DB 110 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 169
 QY 61 DRIFDKTPEP 70
 DB 170 DRIFDKMDEP 179
 NCBI_TaxID=51676;
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RC ROYCE M.E.;
 RL "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR InterPro: IPR001191; Gemin1_AL1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR ProDom: PD000736; Gemin1_AL1; 1.
 DR ProDom: PD000736; Gemin1_AL1; 1.
 FT NON_TER 233 233
 SQ SEQUENCE 233 AA: 26355 MW: AA490AF4D2166A02 CRC64;

Query Match 73.5%; Score 266; DB 12: Length 233;
 Best Local Similarity 68.6%; Pred. No. 4e-21;
 Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Query Match 73.5%; Score 266; DB 12: Length 233;
 Best Local Similarity 68.6%; Pred. No. 4e-21;
 Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLWGEFQVQGAAGCGCOTSDNAAEALNSGTEKALQIIRKIPKYLPOFHNLNSL 60
 DB 110 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 169
 QY 61 DRIFDKTPEP 70
 DB 170 DRIFDKMDEP 179
 NCBI_TaxID=10827;
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOMATO STRAIN.
 RC Guzman R., Giresdonco C.R., Esmatly D., Portillo R.J., Gilbertson R.L.;
 DB EMBL: AF026553; AAR2605.1; -
 DR InterPro: IPR001191; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1; 1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR ProDom: PD000736; Gemin1_AL1; 1.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA: 26486 MW: 9ED8F0697105CD19 CRC64;

Query Match 71.8%; Score 260; DB 12: Length 234;
 Best Local Similarity 67.1%; Pred. No. 1.8e-20;
 Matches 47; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLWGEFQVQGAAGCGCOTSDNAAEALNSGTEKALQIIRKIPKYLPOFHNLNSL 60
 DB 110 TIENGVFQDGSARGSGOOTSDNAAEALNSGTEKAMRIWKELPKFKLPQVHNLSNL 169
 QY 61 DRIFDKTPEP 70
 DB 170 DRIFDKMDEP 179
 NCBI_TaxID=67762;
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-YOKOHAMA3-1;
 RC Ishii T., Yabara T.;
 RL "Molecular phylogeny of geminivirus infecting wild plants in Japan."
 RL J. Plant Res. 110:247-257(1997).
 RL EMBL: AB001315; BAA14033.1; -
 DR InterPro: IPR001191; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1; 1.

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Query Match      71.0%  Score 257.7  DB 12:  Length 190;
Best Local Similarity 58.8%  Pred. No. 3e+20
Matches 50; Conservative 9; Mismatches 10; Indels 16; Gaps 1:

OY 1 TLVGFQVDCAAAGGCGTSHNAAEALNASSKEERLQIIRKIPKYPYQFHNLSNL 60
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Db 85 TLEKCTQIDGRSGGQNDACAALNASSKAKALAIIRKLPKQFYHNLSNL 144
      |||||

OY 61 DRI-----FDRTE 69
      |||||
Db 145 DRIFAPLEVPVCFPTASSDQVPE 169
      |||||

RESULT 14
OQ9827 PRELIMINARY; PRT: 190 AA.
CD OQ9827
DT 01-NOV-1999 (T:LBRL 12, Created)
DT 01-NOV-1999 (T:REMBL 12, Last sequence update)
DT 01-JUN-2001 (T:REMBL 17, Last annotation update)
DE C1 PROTEIN (FRAGMENT).
DE C1
OS Tobacco leaf curl virus.
OC Viruses; ssRNA viruses; Geminiviridae; Begomovirus.

```

[illegible]

Search completed: January 3, 2002, 15:56:24

Fri Jan 4 09:37:40 2002

us-09-289-346a-2.rspt

Page 6

Job time: 1120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:35:03 ; Search time 65.28 Seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346a-2

Perfect score: 362

Sequence: 1 TLWGEFQVQDGAAGGCGT.....POFINLSNLRIDTKTPEP 70

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 0%

Listing first 45 summaries

Database :

1: /cgn2_5/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_5/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_5/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_5/ptodata/2/1aa/6B_COMB.pep.*

5: /cgn2_5/ptodata/2/1aa/6C_COMB.pep.*

6: /cgn2_5/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	215	59.4	353	4	US-08-838-151A-44
2	215	59.4	353	4	US-08-838-151A-46
3	215	59.4	353	4	US-08-838-151A-50
4	215	59.4	353	4	US-08-838-151A-55
5	215	59.4	353	4	US-08-838-151A-55
6	215	59.4	359	4	US-08-809-103B-2
7	215	59.4	359	4	US-08-809-103B-4
8	215	59.4	359	4	US-08-809-103B-6
9	215	59.4	359	4	US-08-809-103B-8
10	213	58.8	361	4	US-08-838-151A-2
11	213	58.8	361	4	US-08-838-151A-6
12	213	58.8	361	4	US-08-838-151A-6
13	213	58.8	361	4	US-08-838-151A-8
14	200	55.2	357	4	US-08-838-151A-24
15	200	55.2	357	4	US-08-838-151A-27
16	200	55.2	357	4	US-08-838-151A-30
17	192	53.0	357	4	US-08-838-151A-20
18	68.5	18.9	1713	3	US-08-600-982-24
19	68.5	18.9	1713	3	US-08-600-982-24
20	65.5	18.1	2161	5	US-07-745-0261A-24
21	65.5	18.1	2161	1	US-08-455-543A-49
22	65.5	18.1	2161	1	US-08-455-543A-51
23	65.5	18.1	2161	2	US-08-223-305C-49
24	65.5	18.1	2161	2	US-08-223-305C-51
25	65.5	18.1	2161	2	US-08-311-363-2
26	63.5	17.5	334	6	5290690-11
27	60	16.6	446	2	US-08-672-614D-11

Sequence 11, Appl
Sequence 31, Appl
Sequence 9, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 23, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 1,4e-19;
; GENERAL INFORMATION:
; APPLICANT: Scout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; INVENTOR: Hanson, Steve
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; TELEPHONE: 312-616-5140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05/08/838,151A
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5140
; TELEFAX: 312-616-5146
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; LENGTH: 353 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-44

Query Match 59.4%; Score 215; DB 4; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFQVQDGAAGGCGTSDNAAALNASSKEEALQITREIKPKYLFQFINLSNL 60

DB 110 TLVGEQFVDGARGGOOSANDSYAKALNADSIETSLTKKEQPKVYLQHNIRSNL 169
QY 61 DRFDKTPPEP 70
DB 170 ERIFVKVPEP 179

RESULT 2

US-08-838-151A-46
Sequence 46, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE: 800
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR DISK: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 59.4%; Score 215; DB 4; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEQFVDGAAAGCQTSNDAAEAALNASKKEPALQIIREKIPKYLQFPHINSNL 60
DB 110 TLVGEQFVDGARGGOOSANDSYAKALNADSIETSLTKKEQPKVYLQHNIRSNL 169
QY 61 DRFDKTPPEP 70
DB 170 ERIFVKVPEP 179

RESULT 3

US-08-838-151A-49
Sequence 49, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE: 800
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR DISK: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 59.4%; Score 215; DB 4; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVGEQFVDGAAAGCQTSNDAAEAALNASKKEPALQIIREKIPKYLQFPHINSNL 60
DB 110 TLVGEQFVDGARGGOOSANDSYAKALNADSIETSLTKKEQPKVYLQHNIRSNL 169
QY 61 DRFDKTPPEP 70
DB 170 ERIFVKVPEP 179

RESULT 4

US-08-838-151A-52
Sequence 52, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/838,151A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

Query Match 59.4%; Score 215; DB 4; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1 TLVWGFQVDCAAAGCGTSDAAARALNASSKEALQIRKPKYLVQHNHNSNL 60
DB 110 TIEMGFQVDCGARGGQSSANDSYAKALNADTSALTLKKEQPKDYVLQHHNRSNL 169
QY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

RESULT 5
US-08-838-151A-55
Sequence 55, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Maxwell, Douglas
APPLICANT: Aniquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Rockey, Milnanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/838,151A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-55

Query Match 59.4%; Score 215; DB 4; Length 353;
Best Local Similarity 57.1%; Pred. No. 1.4e-19;
Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
QY 1 TLVWGFQVDCAAAGCGTSDAAARALNASSKEALQIRKPKYLVQHNHNSNL 60
DB 110 TIEMGFQVDCGARGGQSSANDSYAKALNADTSALTLKKEQPKDYVLQHHNRSNL 169
QY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

RESULT 6
US-08-809-103B-2
Sequence 2, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GHONEMBOHN, Bruno
APPLICANT: INVENTION: TRANSGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94,11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA: NO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US894AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 211-2297
TELEFAX: (703) 211-0575
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 59.4%; Score 215; DB 4; Length 359;
Best Local Similarity 55.1%; Pred. No. 1.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

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QY 2 LVWGEFQVGGAAAGCGQTSNDAAAEALNASSKEALQIREKIPKYLFOFHNLNSLD 61
DB 111 LVNGFTQIDGSRARGGQGTANDAYAKAINAGSKSQALDVIKELAPROYLHFHNLNSLD 170
QY 62 RFDKTPPEP 70
DB 171 KVFQVPPAP 179

RESULT 7
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809.103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; APPLICATION NUMBER: FR 94.11040
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809.103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: WO PCT/FR95/01192
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TEXT: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-4

Query Match 59.4%; Score 215; DB 4; Length 359;
Best Local Similarity 55.1%; Pred. No. 1.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

OY 2 LVWGEFQVGGAAAGCGQTSNDAAAEALNASSKEALQIREKIPKYLFOFHNLNSLD 61
DB 111 LVNGFTQIDGSRARGGQGTANDAYAKAINAGSKSQALDVIKELAPROYLHFHNLNSLD 170
QY 62 RFDKTPPEP 70
DB 171 KVFQVPPAP 179

RESULT 8
US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

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; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809.103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: WO PCT/FR95/01192
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TEXT: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-103B-6

Query Match 59.4%; Score 215; DB 4; Length 359;
Best Local Similarity 55.1%; Pred. No. 1.4e-19;
Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFQVGGAAAGCGQTSNDAAAEALNASSKEALQIREKIPKYLFOFHNLNSLD 61
DB 111 LVNGFTQIDGSRARGGQGTANDAYAKAINAGSKSQALDVIKELAPROYLHFHNLNSLD 170
QY 62 RFDKTPPEP 70
DB 171 KVFQVPPAP 179

RESULT 9
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GROENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

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: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/409,103#
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J, 925
: REFERENCE/DOCKET NUMBER: US894AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: TELEX: 248425 EMBON
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-809-103B-8

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Query Match      59.4%; Score 215; DB 4; Length 359;
Local Similarity 55.1%; Freq: 2.1e-19;
Matches 36; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

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Oy 2 1VWGEFVDGAAAGCGTSDNDAAEALNASSKEALQIIRKIPKYLFPFHNSLND 61
Db 111 1VWGEFVDGAAAGCGTSDNDAAEALNASSKEALQIIRKIPKYLFPFHNSLND 170

Oy 62 RIFDKTPEP 70
Db 171 KVFQVPPAP 179

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RESULT 10
US-08-838-151A-2
: Sequence 2, Application US/08838151A
: Patent No. 6251743
: GENETIC INFORMATION:
: APPLICANT: Slout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60600
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/439,151A

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: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-838-151A-2

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Query Match      58.8%; Score 213; DB 4; Length 361;
Local Similarity 54.3%; Freq: 2.2e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

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Oy 1 1TVWGEFVDGAAAGCGTSDNDAAEALNASSKEALQIIRKIPKYLFPFHNSLND 60
Db 110 1TVWGEFVDGAAAGCGTSDNDAAEALNASSKEALQIIRKIPKYLFPFHNSLND 169

Oy 61 RIFDKTPEP 70
Db 170 ERIFAKAPEP 179

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RESULT 11
US-08-838-151A-4
: Sequence 4, Application US/08838151A
: Patent No. 6251743
: GENETIC INFORMATION:
: APPLICANT: Slout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60600
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein

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US-08-838-151A-4

Query Match 58.8%; Score 213; DB 4; Length 361;
Best Local Similarity 54.3%; Pred. No. 2.6e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
OY 1 TLWGFEVQCGAAGCGCTSDAAAEALINASSKEALQIIRKTPKYLQPHNLNSNL 60
DB 110 TIENGDFQIDRSARGQSQSSYAKALINASSVSQALAVLREEQPKDFVQNHNIISNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 12
US-08-838-151A-6
: Sequence 6, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: FILING DATE: NUMBER: US/08/838, 151A
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5460
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-6

Query Match 58.8%; Score 213; DB 4; Length 361;
Best Local Similarity 54.3%; Pred. No. 2.6e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
OY 1 TLWGFEVQCGAAGCGCTSDAAAEALINASSKEALQIIRKTPKYLQPHNLNSNL 60
DB 110 TIENGDFQIDRSARGQSQSSYAKALINASSVSQALAVLREEQPKDFVQNHNIISNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 13

US-08-838-151A-8
: Sequence 8, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: FILING DATE: NUMBER: US/08/838, 151A
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5460
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-8

Query Match 58.8%; Score 213; DB 4; Length 361;
Best Local Similarity 54.3%; Pred. No. 2.6e-19;
Matches 38; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
OY 1 TLWGFEVQCGAAGCGCTSDAAAEALINASSKEALQIIRKTPKYLQPHNLNSNL 60
DB 110 TIENGDFQIDRSARGQSQSSYAKALINASSVSQALAVLREEQPKDFVQNHNIISNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFAKAPEP 179

RESULT 14

US-08-838-151A-24
: Sequence 24, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milinow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0250
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5400
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: Protein
 US-08-838-151A-24

Query Match 55.2%; Score 200; DB 4; Length 357;
 Best Local Similarity 62.3%; Pred. No. 1.2e-17;
 Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
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 Db 111 FGVSDIGRSGARGGQANDAYAEALNSGKSEALNLKKAPEKDYILOFHNLSNLDRI 170
 Oy 64 F 64
 Db 171 F 171

RESULT 15
 US-08-838-151A-27
 : Sequence 27, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Zhou, Hang
 : APPLICANT: McNeil, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : TITLE OF INVENTION: Genes
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : STREET: Dressler, Rocky, Milinow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC compatible
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/838,151A
 : FILING DATE:
 : CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0250
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5400
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: Protein
 US-08-838-151A-27
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 Best Local Similarity 62.3%; Pred. No. 1.2e-17;
 Matches 38; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
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 Oy 64 F 64
 Db 171 F 171
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 Job time: 225 sec


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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:36 : Search time 144.17 Seconds
(without alignments)
35.965 Million cell updates/sec

Title:
Accession:
Accession score:
Sequences:
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Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description
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1 358 100.0 70 21 AAB18679 Mutant peptide der
2 347 96.9 70 21 AAB18691 Mutant peptide der
3 343 95.8 70 21 AAB18690 Mutant peptide der
4 332 92.7 36 21 AAB18677 Peptide fragment f
5 324 90.5 70 21 AAB18678 Mutant peptide der
6 324 90.5 70 21 AAB18688 Mutant peptide der
7 321 89.7 70 21 AAB18688 Mutant peptide der
8 320 89.4 70 21 AAB18692 Mutant peptide der
9 318 88.8 70 21 AAB18684 Mutant peptide der
10 317 88.5 70 21 AAB18678 Mutant peptide der
11 317 88.5 70 21 AAB18686 Mutant peptide der

12 316 88.3 70 21 AAB18689 Mutant peptide der
13 314 87.7 70 21 AAB18680 Mutant peptide der
14 311 86.9 70 21 AAB18681 Mutant peptide der
15 310 86.6 70 21 AAB18683 Mutant peptide der
16 308 86.0 70 21 AAB18682 Mutant peptide der
17 308 86.0 36 18 AAB18677 Peptide fragment f
18 218 60.9 36 18 AAB18678 Mutant peptide der
19 218 60.9 36 18 AAB18688 Mutant peptide der
20 218 60.9 36 18 AAB18692 Mutant peptide der
21 217 60.6 35 18 AAB18692 Mutant peptide der
22 217 60.6 35 18 AAB18692 Mutant peptide der
23 217 60.6 35 18 AAB18692 Mutant peptide der
24 217 60.6 35 18 AAB18692 Mutant peptide der
25 217 60.6 35 18 AAB18692 Mutant peptide der
26 215 60.1 35 8 AAP70407 ORF 4 gene product
27 212 59.2 35 17 AAB88870 Sardinian tomato y
28 212 59.2 35 17 AAB88871 Sardinian tomato y
29 212 59.2 35 17 AAB88872 Product of ORF 4 f
30 200.5 56.0 36 18 AAP70562 Tobacco and cutt
31 198 53.1 36 18 AAP70562 Tobacco and cutt
32 198 53.1 36 18 AAP70562 Tobacco and cutt
33 190 53.1 35 18 AAB18677 Peptide fragment f
34 190 53.1 35 18 AAB18678 Mutant peptide der
35 190 53.1 35 18 AAB18688 Mutant peptide der
36 73.5 20.5 304 22 AAB19860 Human polyptide
37 73.5 20.5 406 22 AAB19860 Human polyptide
38 73.5 20.5 425 22 AAB74314 Human splicing fac
39 73.5 20.5 425 22 AAB74314 Human splicing fac
40 63.5 17.5 579 16 AAB53700 Human polyptide
41 61.5 17.2 66 11 AAB08067 Synthetic antifere
42 61 17.0 197 21 AAG24212 Arabidopsis thalia
43 61 17.0 218 21 AAG24211 Arabidopsis thalia
44 61 17.0 1212 20 AAB88287 Rat (Na.K)-ATPase
45 61 17.0 1212 20 AAB88288 Rat (Na.K)-ATPase

ALIGNMENTS

RESULT 1
AAB18679
ID AAB18679 standard; peptide; 70 AA.
FT AAB18679;
XX AAB18679;
DT 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX Ribosome binding region; resistance: geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 27 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 30 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 34 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 35 /note= "wild type residue replaced with Ala"
XX
XX Misc-difference 36 /note= "wild type residue replaced with Ala"
XX
XX WC200054573-AL.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-US06759.

```


XX		18-MAR-1999:	9905-0125004.	
PR		09-APR-1999:	9905-0289346.	
XX		(UYNC-) UNIV NORTH CAROLINA STATE.		
XX		Hanley-Bowdoin L, Orozco BM, Kong L;		
XX		WPI: 2000-618851/59.		
DR		Disclosure; Page 18; 73pp; English.		
XX		The present sequence is derived from a geminivirus replication (Rep)		
XX		protein, which is also known as ALI. ALI binds double-stranded DNA,		
CC		catalyses cleavage and ligation of single-stranded DNA, and interacts		
CC		with other viral and host proteins. Mutants of the ALI protein are used		
CC		to produce transgenic plants. The mutation in ALI present in mutants		
CC		is between binding sites for expression of m... At plant leaves,		
CC		increased resistance to geminivirus infection in the plant. Mutant ALI		
CC		proteins are useful for producing plants having increased resistance or		
CC		reduced sensitivity to a geminivirus such as tomato golden mosaic virus,		
CC		tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl		
CC		virus, African cassava mosaic virus, Indian cassava mosaic virus, potato		
CC		yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,		
CC		squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or		
XX		beet curly top virus.		
XX		Sequence 70 AA:		
SO				
		Query Match 92.7%; Score 332; DB 21; Length 70;		
		Best Local Similarity 92.9%; Pred. No. 7e-36; 5; Indels 0; Gaps 0;		
		Matches 65; Conservative 0; Mismatches 5;		
OY		1 TLVWGEPQVDGRSANGCQTSDNDAAMALAGSAAALQITREKIPKYLPQHFNHNSL 60		
Db		1 tlwgeqfvdvrgsgcqtndaaealnasskealqlirekipekylfqhfnlnsl 60		
OY		61 DRIFETPPFP 70		
Db		61 drifktcpfp 70		
		RESULT 5		
AAAB18687		AAAB18687		
ID		AAB1B687 standard; peptide: 356 AA.		
AC		AAB1B687;		
AD		22-JAN-2001 (first entry)		
DE		Amino acid sequence of a geminivirus replication protein of TGMV.		
KX		Geminivirus; replication protein; Rep protein; ALI; transgenic plant;		
KW		ribosome binding region; resistance; geminivirus infection.		
OS		Tomato golden mosaic virus.		
CS		Key Location/Qualifiers		
FT		Misc-difference 354		
FT		/note= "unspecified amino acid"		
XX		WO200054573-A1.		
XX		21-SEP-2000.		
PF		15-MAR-2000; 2000MO-US06759.		

PR 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant Ail protein with a mutation in the Rb binding region
 PT
 XX
 XX Disclosure: Page 47-48; 73pp; English.
 XX
 CC The present sequence represents a geminivirus replication (Rep)
 CC protein, which is also known as Ail. Ail binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the Ail protein are used
 CC in transgenic plants. The mutation in Ail is present in a
 CC ribosome binding site, expected to increase resistance to geminiviruses.
 CC Increased resistance to geminivirus infection in the plant. Mutant Ail
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC cassava leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX
 XX Sequence 356 AA:

Query Match 92.7%; Score 332; DB 21; Length 356;
 Best Local Similarity 91.5%; Pred. No. 7:4e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 60
 110 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 169
 DB 110 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 169
 OY 61 DRIPKTPPEP 70
 110 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 169
 DB 170 DRIPKTPPEP 179

RESULT 6
 AAB18685
 ID AAB18685 standard; peptide: 70 AA.
 XX
 XX AAB18685;
 XX
 DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (Ail) protein.
 XX
 XX Geminivirus; replication protein; Rep protein; Ail; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 19 /note- "wild type residue replaced with Ala"
 FT
 FT
 FT
 PN WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX

PR 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant Ail protein with a mutation in the Rb binding region
 PT
 XX
 XX Claim 53; Page 46; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as Ail. Ail binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the Ail
 CC protein are used to produce transgenic plants. The mutation in Ail is
 CC in a ribosome binding site, expected to increase resistance to geminiviruses.
 CC Increased resistance to geminivirus infection in the plant. Mutant Ail
 CC proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, cassava leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA:

Query Match 90.5%; Score 324; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 7:7e-35;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 60
 1 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 60
 DB 1 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 60
 OY 61 DRIPKTPPEP 70
 1 TLVWGEFQVDRSGRGCGTSDNAAAAAALASSAAALQIIREKIPKYLFOFHNSNL 60
 DB 61 DRIPKTPPEP 70

RESULT 7
 AAB18688
 ID AAB18688 standard; peptide: 70 AA.
 XX
 XX AAB18688;
 XX
 DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (Ail) protein.
 XX
 XX Geminivirus; replication protein; Rep protein; Ail; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 19 /note- "wild type residue replaced with Ala"
 FT
 FT
 FT
 PN WO200054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX

15-MAR-2000; 2000WO-US06759.

18-MAR-1999; 99US-0125004.
09-APR-1999; 99US-0289346.

(UWNC)- UNIV NORTH CAROLINA STATE.

Hanley-Bowdoin L, Orozco BM, Kong LJ;
MPI: 2000-618851/59.

Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant ALI protein with a mutation in the Rb-binding region .

Disclosure: Page 48; 73pp: English.

The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as ALI. ALI binds double-stranded DNA, catalyzes cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the ALI gene have been generated which are resistant to geminivirus infection. This present in a ribosome binding region, and expression of mutant ALI protein imparts increased resistance to geminivirus infection in the plant. Mutant ALI proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, cucumber greening virus, "ashby" virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA:

Query Match 89.7%; Score 321; DB 21; Length 70;
Best Local Similarity 90.0%; Pred. No. 1.9e-34;
Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TLWGKQVQDNGRGCGCTSDNAAALAAASSAAAAQTIREKIPEKYLPQPINNSNL 60
DB 1 tllwgkfvgdrsggcaasdaaealnasskeelqirekipekylfqfhtlnsl 60

OY 61 DRIFDKTPEP 70
DB 61 drifdktpgp 70

RESULT 8
ID AAB18692 standard; peptide: 70 AA.
XX CC XC
XX CC XC
XX CC XC
DT DT XX
DE DE XX
XX DE XX
KK KK WW
RW RW KW
XX GS
OS OS
OS OS
Key Location/Qualifiers
FF FF
FT FT Misc-difference 66
FT FT /note= *wild type residue replaced with Ala"
FT FT Misc-difference 69
XX XX /note= *wild type residue replaced with Ala"
PN PN
XX WO200054573-A1.

[illegible]

PN WO200054573-A1.
 PD 21-SEP-2000.
 PT 15-MAR-2000: 2000WO-US06759.
 PT 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI: 2000-618851/59.
 PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT .
 XX Claim 52: Page 45; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 XX geminivirus replication (Rep) protein, also known as A11. A11 binds
 XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 XX DNA, and interacts with other viral and host proteins. Mutants of the A11
 XX protein are used to produce transgenic plants. The mutation in A11 is
 XX present in a ribosome binding region, and expression of the mutant A11
 XX protein imparts increased resistance to geminivirus infection in the
 XX plant. Mutant A11 proteins are useful for producing plants having
 XX increased resistance or reduced sensitivity to a geminivirus such as
 XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 XX virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ
 Query Match 88.8%; Score 318; DB 21; Length 70;
 Best Local Similarity 90.0%; Pred. No. 4.7e-34;
 Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 1 TLVWGFQVDCRGAGCGCTSDNAAAALAAASSAAALQIREKIPKYLQFPHNLSNL 60
 DB 1 tlvwgeavdgragrgcgtcsndaaalnasskeaalqirekipekylqfphnlsnl 60
 QY 61 DRIFDKTPEP 70
 DB 61 drifdktp 70
 RESULT 10
 AAB18578
 ID AAB18678 standard; peptide: 70 AA.
 AC AAB18678;
 DT 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus; replication protein; Rep protein: A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 PH Key Location/Qualifiers
 FT Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13

FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 15 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000: 2000WO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI: 2000-618851/59.
 PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT .
 XX Claim 53: Page 42-43; 73pp; English.
 XX The present sequence represents a mutant peptide, derived from a
 XX geminivirus replication (Rep) protein, also known as A11. A11 binds
 XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 XX DNA, and interacts with other viral and host proteins. Mutants of the A11
 XX protein are used to produce transgenic plants. The mutation in A11 is
 XX present in a ribosome binding region, and expression of the mutant A11
 XX protein imparts increased resistance to geminivirus infection in the
 XX plant. Mutant A11 proteins are useful for producing plants having
 XX increased resistance or reduced sensitivity to a geminivirus such as
 XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 XX virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ
 Query Match 88.5%; Score 317; DB 21; Length 70;
 Best Local Similarity 88.6%; Pred. No. 6.3e-34;
 Matches 62; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 OY 1 TLVWGFQVDCRGAGCGCTSDNAAAALAAASSAAALQIREKIPKYLQFPHNLSNL 60
 DB 1 tlvwgeivdgragrgcgtcsndaaalnasskeaalqirekipekylqfphnlsnl 60
 QY 61 DRIFDKTPEP 70
 DB 61 drifdktp 70
 RESULT 11
 AAB18686
 ID AAB18686 standard; peptide: 70 AA.
 AC AAB18686;
 DT 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus; replication protein; Rep protein: A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 PH Key Location/Qualifiers
 FT Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13

```

FH Key Location/Qualifiers
FT Misc-difference 24
FT FT Misc-difference 22 /note= "wild type residue replaced with Leu"
FT FT Misc-difference 22 /note= "wild type residue replaced with Leu"
FT FT Misc-difference 26 /note= "wild type residue replaced with Leu"
FT FT Misc-difference 26 /note= "wild type residue replaced with Leu"
XX XX
XX W0200054573-AL.
XX XX
XX 21-SEP-2000.
XX XX
XX 15-MAR-2000; 2000MO-US06759.
XX XX
XX 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AII protein with a mutation in the Rb binding region
XX FT
XX PS Claim 53; Page 46; 73pp; English.
XX XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AII. AII binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AII
XX protein are used to produce transgenic plants. The mutation in AII
XX present in the ribosome binding region, and expression of mutant AII
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AII proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX XX
XX Sequence 70 AA;
XX
XX Query Match 88.5%; Score 317; DB 21; Length 70;
XX Best Local Similarity 88.5%; Pred. No. 8, 6e-34; 8; Indels 0; Gaps 0;
XX Matches 62; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX Oy 1 TLVGFQVQDGRSARGGCTSDNAAAALAASSAAAALQIREKIPKYLQFQHNLSNL 60
XX Db 1 tlvgvqfvgdrgsarggctsdnlllealnasskeaalqirekipekylqfghnlnsl 60
XX
XX Oy 61 DRFDKTPPEP 70
XX Db 61 drfdktpep 70
XX
XX RESULT 12
XX AAB18689
XX ID AAB18689 standard; peptide; 70 AA.
XX AC AAB18689;
XX XX
XX 22-JAN-2001 (first entry)
XX XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AII) protein.
XX DE Geminivirus; replication protein; Rep protein; AII; transgenic plant;
XX XX ribosome binding region; resistance; geminivirus infection.
XX

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XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX PR Key Location/Qualifiers
XX FT Misc-difference 22 /note= "wild type residue replaced with Ala"
XX FT FT Misc-difference 23 /note= "wild type residue replaced with Ala"
XX FT FT
XX XX W0200054573-AL.
XX XX
XX 21-SEP-2000.
XX XX
XX 15-MAR-2000; 2000MO-US06759.
XX PF
XX 18-MAR-1999; 99US-0125004.
XX PR 09-APR-1999; 99US-0289346.
XX XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AII protein with a mutation in the Rb binding region
XX FT
XX PS Disclosure; Page 48-49; 73pp; English.
XX XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AII. AII binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AII
XX protein are used to produce transgenic plants. The mutation in AII
XX present in a ribosome binding region, and expression of mutant AII
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AII proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX XX
XX Sequence 70 AA;
XX
XX Query Match 88.3%; Score 316; DB 21; Length 70;
XX Best Local Similarity 90.0%; Pred. No. 8, 6e-34;
XX Matches 63; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX Oy 1 TLVGFQVQDGRSARGGCTSDNAAAALAASSAAAALQIREKIPKYLQFQHNLSNL 60
XX Db 1 tlvgvqfvgdrgsarggctsdnlllealnasskeaalqirekipekylqfghnlnsl 60
XX
XX Oy 61 DRFDKTPPEP 70
XX Db 61 drfdktpep 70
XX
XX RESULT 13
XX AAB18680
XX ID AAB18680 standard; peptide; 70 AA.
XX AC AAB18680;
XX XX
XX 22-JAN-2001 (first entry)
XX XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AII) protein.
XX DE Geminivirus; replication protein; Rep protein; AII; transgenic plant;
XX XX ribosome binding region; resistance; geminivirus infection.
XX

```


GenCode version 4.5
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OW protein - protein search, using sw model

Run on: January 3, 2002, 15:40:08 : Search time 72.79 seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346a-3

Perfect score: 358

Sequence: 1 TLVNGFQVDSRGSGCQT.....TFPHNLSNLDRIKDTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	92.7	352	1 QOCV11	Al1 protein - toma
2	243	67.9	361	1 QOCVPT	Al1 protein - pota
3	230	64.2	358	2 S07594	hypothetical prote
4	222	62.0	362	1 J01887	Al1 protein - toma
5	217	60.6	355	1 QOCVW1	AV1 protein - abut
6	216	60.3	349	2 S13165	replicase - pepper
7	216	60.3	349	2 S13165	replicase - pepper
8	216	60.3	359	2 S39211	gene Cl protein -
9	214	59.8	358	1 J01870	Al1 protein - toma
10	213	59.5	351	2 J02327	Al1 protein - indi
11	212	59.2	359	2 S22593	hypothetical prote
12	208	58.1	385	2 S28360	Al1 protein - beet
13	207	57.8	360	2 S59885	replication-associ
14	203	56.7	357	2 S32235	gene Cl protein -
15	203	56.7	357	2 S32235	Al1 protein - toma
16	120	33.5	131	2 S45059	Al1 protein (clon
17	115	32.1	347	1 QOCV81	Al1 protein - squa
18	69	19.3	377	2 Q30237	transcription init
19	66	18.4	508	2 S59870	fork head domain p
20	66	18.4	508	2 S59870	probable large ATP
21	65	18.2	671	2 A35912	homeotic protein o
22	63	17.6	782	2 T44362	acetyl-CoA C-acety
23	63	17.6	782	2 T44362	acetyl-CoA C-acety
24	62.5	17.3	1077	2 A44067	Spliceosome-associ
25	62	17.3	409	2 T16781	hypothetical prote
26	61.5	17.2	327	2 F83408	hypothetical prote
27	61.5	17.2	705	2 T31157	hypothetical prote
28	61.5	17.2	1541	2 T02831	AAA protein I4171
29	61	17.0	339	2 T26328	hypothetical prote

30	61	17.0	371	2 B95052	alcohol dehydrogen
31	61	17.0	1265	2 T47626	structural main ten
32	61	17.0	1510	2 T33100	hypothetical prote
33	60.5	16.9	899	2 A34692	O-succinylhomoseri
34	60.5	16.9	899	2 A34692	purif 74E protein -
35	60.5	16.9	883	2 S04722	paired type homeob
36	60	16.8	314	2 JC5273	probable flagellar
37	59.5	16.6	201	2 A81380	hypothetical prote
38	59.5	16.6	244	2 B86197	gamma-aminobutyrat
39	59.5	16.6	470	2 T46814	probable phosphos
40	59.5	16.6	461	2 A70091	ubiquitin-like prote
41	59.5	16.6	380	2 S70594	ubiquitin-cytochr
42	59	16.5	380	2 S70594	calcitonin recept
43	59	16.5	482	2 A92485	calcitonin recept
44	59	16.5	498	2 I47130	5-aminolevulinate
45	59	16.5	513	1 SYCHLE	

ALIGNMENTS

RESULT 1
QOCV11
C:Species: tomato golden mosaic virus
A:Note: Host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #text-change 08-Apr-1994
P:Hamilton, W.D.O.; Steilo, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 352 <GAP>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus Al1 protein

Query Match 92.7% Score 332 DB 1 Length 352:
Best Local Similarity 92.9% Prev No 7 2e-31:
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0:

Qy 1 TLVNGFQVDSRGSGCQTSDNAAAALAAASAAALQITREIKPKYLFQPHNLSNL 60
|||||
Db 111 TLVNGFQVDSRGSGCQTSDNAAAALAAASAAALQITREIKPKYLFQPHNLSNL 170
|||||

Qy 61 DRIEIKTPEP 70
|||||

Db 171 DRIEIKTPEP 180
|||||

RESULT 2

QOCVPT
C:Species: potato yellow mosaic virus (isolate Venezuela)
A:Note: Host Nicotiana glauca
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 16-Jun-2000
P:Coats, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; MUID:91311403
A:Accession: J00364
A:Residues: 1-361 <COU>
A:Residues: 1-361 <COU>
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:g222458; PIDN:BAA00782.1; PTD:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus Al1 protein

RESULT 7
S31875
All protein - pepper rikizado amarillo virus

A:Residues: 1-358 <ABO>
A:Cross-references: GB:IL14450
C:Genetics:
C:Map position:
C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.5%; Score 214; DB 1: Length 358;
Best Local Similarity 55.7%; Pred. No. 3,5e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLWGEFQVGRSGCGTSDNAAAAAALAAASAAALQIIREKIPKLYQFHNLSML 60
DB 107 TLWGEFQVGRSGCGTSDNAAAAAALAAASAAALQIIREKIPKLYQFHNLSML 166
QY 61 DRIFQKTPPEP 70
DB 167 ERIFAKAPEP 176

RESULT 10
JQ232:protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Species: Indian cassava mosaic virus
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
C:Accession: JQ2327; S35883
R:Hong, Y.G.; Robinson, D.J.; Hartison, B.O.
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-t
A:Accession: JQ2327
A:Reference: PMID:34085070
A:Molecule type: DNA
A:Residues: 1-351 <RDN>
C:Cross-references: EMBL:224758; NID:9393351; PIDN:CA480891.1; PID:g584046
C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.5%; Score 213; DB 2: Length 351;
Best Local Similarity 55.7%; Pred. No. 4e-17;
Matches 41; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 4 WGEFQVGRSGCGTSDNAAAAAALAAASAAALQIIREKIPKLYQFHNLSMLDRI 63
DB 113 WGEFQVGRSGCGTSDNAAAAAALAAASAAALQIIREKIPKLYQFHNLSMLDRI 172
QY 64 FDKTPPEP 70
DB 173 FTKPPPP 179

RESULT 11
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C:Accession: S22593
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
R:Khey-Pour, A.; Bendahmane, M.; Matzke, V.; Accotto, G.P.; Crespi, S.; Gronenborn,
Nucleic Acids Res. 19, 6763-6769, 1991
A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monoep
A:Reference number: S22588; MUID:9107660
A:Accession: S22593
A:Molecule type: DNA
A:Title: Preliminary nucleic acid sequence not shown; translation not shown
A:Residues: 1-359 <RHE>
C:Cross-references: EMBL:X61153; NID:g62211; PIDN:CA43466.1; PID:g62217
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C:Superfamily: tomato golden mosaic virus All protein

Query Match 59.2%; Score 212; DB 2: Length 359;
Best Local Similarity 56.3%; Pred. No. 4e-17; 20;
Matches 39; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

```

QY      2 LVWGFEQWDRSGRCGCGTNSNDAAAALAASSAAAAAQIIIREKYPKEFHNLSNLD   61
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     111 LEWGFTFDGRSGRGQGTANDAKAINAGSKSQALDVKELAPDYVLFHFINSNLD 170

QY     62 RIFDKTPSP 70
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    171 KVFQVPFP 179

RESULT 12
A1:Protein - beet curly top virus
A1:Accession: S28360
C1:Species: beet curly top virus
C1:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
R1:Stanley, J.; Markham, P.G.; Callis, R.J.; Plimmer, M.S.
A1>Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top virus
A1:Reference number: S28360
A1:Accession: S28360
A1>Status: translation not shown
A1:Molecule type: DNA
A1:Source: SV40
C1:Cross-references: GB:M24597; EMBL:X04144; NID:g210678; PIDN:AAA42751.1; PID:g210679
C1:Superfamily: tomato golden mosaic virus A1:protein

```

Query Match 58.1%; Score 208; DB 2; Length 385;
Best Local Similarity 55.7%; Pred. No. 1.9e-16;
Matches 39; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy	1	TLWGEFQVDRSGRGCGTSDNDMAAALASAAALQITREKPEKYLFQFHNLNSML	60
Db	137	TIWGEFQVDRSGRGCGTSDNDMAAALASAAALQITREKPEKYLFQFHNLNSML	196
Qy	61	DRIFDKTPEF 70	
Db	197	QKIFORPPEP 206	

RESULT 13
S59885
S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: S59885
R:Hong, Y.; Harrison, B. D.
submitted to the EMBL Data Library, February 1995
A:Description: Nucleotide sequences from tomato leaf curl viruses from different
d geminiviruses.
A:Reference number: S59346
A:Accession: S59885
A:Accession: S59885
A:Molecule type: Primary
A:Molecule type: DNA
A:Residues: 1-360 <HON>
A:Cross-references: EMBL:248182; NID:G944538; PIDN:CA688229,1; PID:G974211
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 57.8%; Score 207; DB 2; Length 360;
Best Local Similarity 60.6%; Pred. No. 2.3e-15;
Matches 40; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY	4	WGDFVGDSRGSGCGQTSDNDAAAALANASSNAALQITREKIPKYLFPQHNLNSLNDRI	63
DB	113	FVGVIGDGSARGGQSANDAYAEINSGSKAAALDLIREAKPKDFVLQFPHNLNLDRI	172
QY	64	FDKTPE	69
DB	173	FTPSAE	178

RESULT 14

S39235
gene c1 protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
A:Accession: S39235
A:Author: G. Valsecchi, A. Passco, D. Accotto, G.
submitted to the EMBL Data Library, December, 1993
A:Description: A cloned DNA from a TMVc isolate from Sicily showing low infectivity.
A:Reference number: S39233
A:Accession: S39235
A>Status: preliminary
A:Molecule type: DNA
A:Length: 355 bp
A:Cross-references: EMBL:228390; NID:g1041571; PID:g1334964
C:Superfamily: tomato golden mosaic virus ML1 protein

Query Match 56.7%; Score 203; DB 2; Length 359;
Best Local Similarity 53.6%; Pred. No. 6.6e-16;
Matches 37; Conservative 12; Mismatches 20 Indels

QY 2 LWGEFQVDSARGCOTSDNDAAMALAASSAAAALQIIRKXPEKYLQFHNLNSLND 61
 | ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Dd 111 LEWGTFQIDSGARGGOOTANDAYAKAINARSKSEALDVIKQAPROYVLVLFHNISSLD 170

QY 62 RIFDKTPEP 70

Db 171 KVFOVPPAP 179

RESULT 15

AL1 protein - tomato yellow leaf curl virus
 A:Alternate names: C1 protein
 C:Species: tomato yellow leaf curl virus
 C:Date: 30-Jun-1992 sequence_revision 30-Jun-1992
 C:Accession: A040779
 R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.
 Virology 185, 151-161, 1991
 A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
 A:Reference number: A040779; UID: 92024070

A;Residues: 1-35/ <NAV>
A;Cross-references: GB:X15656; NID:g62204; PIDN:CAA33688.1; PID:g62207
C:Superfamily: tomato golden mosaic virus All protein

Query Match 53.1%; Score 190; DB 1; Length 357;
Best Local Similarity 60.7%; Pred. No. 2.le-14;
Matches 37: Conservative 11; Mismatches 13; Indels

[illegible]

Qv 64 F 64

Db 171 F 171

Search completed: January 3, 2002, 15:40:08
Job time: 304 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: January 3, 2002, 15:57:14 ; Search time 43.68 Seconds
(without alignments)
58,758 Million cell updates/sec

Title: US-09-289-346a-3
P: 350
Sequence: 1 TLWGFQVDSARGGCQT.....QFHNLSNLDRIEDKTEEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_39;+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	92.7	352	1 VAL1_TGMV	P03567 tomato gold
2	243	67.9	361	1 VAL1_PMYV	P27258 potato yell
3	243	67.9	361	1 VAL1_PMYV	P27258 potato yell
4	230	64.2	358	1 VAL1_GLYN	P14572 cassava lat
5	222	62.0	362	1 VAL1_TYLCV	P36279 tomato yell
6	217	60.6	355	1 VAL1_ABYMV	P21947 abutilon mo
7	216	60.3	349	1 VAL1_PMYV	P06523 pepper huas
8	216	60.3	359	1 VAL1_TYLCV	P38609 tomato yell
9	215	60.1	353	1 VAL1_BGMV	P05175 bean golden
10	212	59.2	359	1 VAL1_TYLCV	P27260 tomato mott
11	212	59.2	359	1 VAL1_TYLCV	P27260 tomato mott
12	208	58.1	358	1 VAL1_BCTV	P14991 beet curly
13	190	53.1	357	1 VAL1_TYLCV	P27259 tomato yell
14	115	32.1	347	1 VAL1_SICV	P29048 squash leaf
15	69	19.3	377	1 T2FA_DRONE	O05913 drosophila
16	66	18.4	207	1 IUG_MARMO	O35736 marmota mon
17	66	18.4	207	1 CROC_DRONE	P22027 drosophila
18	66	18.4	207	1 CROC_DRONE	P22027 drosophila
19	62.5	17.5	1077	1 HLES_DRONE	O22309 drosophila
20	60.5	16.9	829	1 E74A_DRONE	P20105 drosophila
21	60.5	16.9	883	1 E74B_DRONE	P11536 drosophila
22	60.5	16.9	883	1 E74B_DRONE	P11536 drosophila
23	60.5	16.9	883	1 E74B_DRONE	P11536 drosophila
24	59.5	16.6	470	1 PKXB_MOUSE	O35690 mus muscu
25	59	16.5	379	1 RYLA_MOUSE	O9232 rhizobium m
26	59	16.5	379	1 RYLA_MOUSE	O9232 rhizobium m
27	59	16.5	379	1 RYLA_MOUSE	O9232 rhizobium m
28	59	16.5	379	1 RYLA_MOUSE	O9232 rhizobium m
29	58.5	16.3	1264	1 MOLR_ECOLI	P33345 escherichia
30	58.5	16.3	1713	1 LNA3_HUMAN	O16787 homo sapien
31	58	16.2	732	1 CYG4_HUMAN	P33402 homo sapien
32	58	16.2	1081	1 UL52_HSVB	P28962 equine herp
33	58	16.2	1952	1 TR12_HUMAN	Q14669 homo sapien

P10593 zea mays (m)
P31277 homo sapien
Q04791 anas platyr
Q99856 homo sapien
Q62431 mus muscu
P27552 human papil
P09065 mus muscu
P18479 2 genome po
P39105 saccharomyc
P55012 mus muscu
Q44010 leishmania

ALIGNMENTS

RESULT 1
VAL1_TGMV TGMV STANDARD: PRT; 352 AA.
AC P03567
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AC1
CS Tomato golden mosaic virus (TGMV).
CC Uses: ssDNA viruses; Geminiviridae; Begomovirus.
CC NCBI_TaxID=10531;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT *Complete nucleotide sequence of the infectious cloned DNA components
RT of tomato golden mosaic virus: potential coding regions and regulatory
RT sequences. J. Virol. 57:2205(1984).
CC
CC - - - SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY
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CC
CC EMBL: K02029; -; NOT_ANNOTATED_CDS.
DR PIR: A04170; Q0CVLL.
DR InterPro: IPR001151; Gemin_A1.
DR Pfam: PF00095; Gemin_A1.1.
DR PRINTS: PR00228; GEMIN_A1.
DR PRODOM: PD000736; Gemin_A1.1.
KW ATP-binding.
FT NP_BIND 223 230 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C3C9C38F5644B4A CRC64:

Query Match 92.7%; Score 332; DB 1; Length 352;
Best Local Similarity 92.9%; Pred No. 4, 1e-31;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TLWGFQVDSARGGCQTSDNAAAALAAASAAALQIREIKPEKLYQFHNLSN 60
Db 111 TLWGFQVDSARGGCQTSDNAAAALAAASAAALQIREIKPEKLYQFHNLSN 170
Qy 61 DRIEDKTEEP 70
Db 171 DRIEDKTEEP 180

RESULT 2
VAL1_PMYV

DB	169	DRIFCEPAP	178
RESULT	4		
VALID_CLVN		STANDARD;	PRT; 358 AA.
ID	VALI_CLVN		
DT	19977		
DT	01-APR-1990	(Rel. 14, Created)	
DT	01-APR-1990	(Rel. 14, Last sequence update)	
DT	01-JUN-1994	(Rel. 28, Last annotation update)	

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CC	-----	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	-----	or send an email to license@isb-sib.ch).	
CC	-----		
DR	EMBL: X17095; G0534353.1; -		
DR	PIR: S07594; S07594		
DR	InterPro: IPR001191; Gemini_AL1.		
DR	Pfam: PF00799; Gemini_AL1; 1.		
DR	PRINTS: PR00227; GEMCATCLV1.		
DR	PRINTS: PR00228; GEMCATCLV1.		
DR	ProDom: PD000736; Gemini_AL1; 1.		
DR	ATP-binding: 220 227		
KW	ATP-BINDING		
FT	SEQUENCE 358 AA; 40435 MW; 1DB1BB0C32552C CNO64;		
EQ			

Query Match	64.2%	Score 230;	DB 1;	Length 358;
Best Local Similarity	60.0%;	Pred. No. 2.6e-19;		
Matches 42:	Conservative	13;	Mismatches 15;	Indels 0;
Gaps	0;			

```

Oy 1 TLVWGFQVQDSARGSCOTSDNAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
    l:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 TVWGFQVQDSARGSCOTSDNAAALAAASSAAALQIIREKIPKYLQFHNLSNL 169
Oy 61 DRIFDKTEP 70
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 DRIFQEPAP 178
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
ID VAL1_ABMW STANDARD; PRT; 362 AA.
DR P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
GN C1.
OR "The yellow leaf curl virus (strain Australia) (TYLCV).
OC VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=36447;
RM -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Ridgen J.E., Krake L.R., Mullineux P.M., Rezaian M.A.:
RT Nucleotide sequence and genome organization of tomato leaf curl
    geminivirus. J. Gen. Virol. 74:147-151(1993).
PL 3 Gen. Virol. 74:147-151(1993).
DR -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR PIR: JQ1887; JQ1887.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00759; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRODOM: PD00228; GEMCOATL1.
DR PIR: JQ1887; JQ1887.
DR ATP-Binding. 221 228 ATP (POTENTIAL).
FP NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41157 MW; 343E7184B4704098 CRC64;

Query Match 52.0%; Score 222; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 2.2e-18;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

Oy 1 TLVWGFQVQDSARGSCOTSDNAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
    l:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWGFQVQDSARGSCOTSDNAAALAAASSAAALQIIREKIPKYLQFHNLSNL 169
Oy 61 DRI-----FKTKTE 69
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRITPPYVVSFLSSDFNVE 194
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
ID VAL1_ABMW STANDARD; PRT; 355 AA.
DR P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AC1.
OR Abutilon mosaic virus (isolate West India).
OC VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=10516;
RM -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
RX MEDLINE=91020984; PubMed=2219703;
RA Frieschmuth T., Zimmat G., Jeske H.:
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
    as well as eukaryotic features."
    Virology 178:461-469(1990).

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-1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL; X15983; -. NOT_ANNOTATED_CDS.
DR PIR: A36214; A36214.
DR Pfam: PF00759; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRODOM: PD000736; Gemini_AL1; 1.
KW ATP-Binding. 221 228 ATP (POTENTIAL).
FP NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40257 MW; 1GACAB6A3251E95 CRC64;

Query Match 60.6%; Score 217; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. No. 8.3e-18;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Oy 1 TLVWGFQVQDSARGSCOTSDNAAALAAASSAAALQIIREKIPKYLQFHNLSNL 60
    l:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TAEWGFQVQDSARGSCOTSDNAAALAAASSAAALQIIREKIPKYLQFHNLSNL 169
Oy 61 DRIFDKTEP 70
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 ERIFAKAPEP 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
ID VAL1_PHVU STANDARD; PRT; 349 AA.
OC Q06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN P.
OR Pepper huasteco virus (PHV).
OC VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxID=28349;
RM -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco L., Garzon-Viznado J.A., Herrera-Estrella L.,
    "Complete nucleotide sequence of pepper huasteco virus: analysis and
    comparison with bipartite geminiviruses."
    J. Gen. Virol. 74:2225-2231(1993).
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CC EMBL; X70418; CAA49856.1;
DR PIR: S31875; S31875.
DR TIR: 023001; 023001.
DR Pfam: PF00759; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCOATL1.
DR PRODOM: PD000736; Gemini_AL1; 1.

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KW ATP-binding. 221 228 ATP (BY SIMILARITY).
FT NP_BIND 221 228
SQ SEQUENCE 349 AA; 39722 MW; 5DFAE76CD5370F4 CRC64;

Query Match
Best Local Similarity 58.3%; Score 216; DB 1; Length 349;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Oy 1 TLVGEFQVDSARGSGCOTSDNAAALAAASAAALQITREKIPKYLQPHNLSNL 60
Db 110 TLVGEFQVDSARGSGCOTSDNAAALAAASAAALQITREKIPKYLQPHNLSNL 60
Oy 61 DRIFKTPPEP 70
Db 170 NRIFQTPPEP 179

RESULT 9
ID VAL1_BGMV STANDARD; PRT; 353 AA.
AC P05175;
DT 13-AUG-1987 (Rel. 05, Created)
DR 01-JUN-1994 (Rel. 29, Last annotation update)
DT 01-OCT-1994 (Rel. 34, Last annotation update)
DE AL1 PROTEIN (40.2 KDA PROTEIN).
GN AC1.
OS Bean golden mosaic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
Ox NCBI_TaxID=10839;
Rw SEQUENCE FROM N.A.
Rt Hoonorth A.J., Caton J., Bossert M., Goodman R.M.;
RA "Nucleotide sequence of bean golden mosaic virus and a model for gene
RL regulation in geminiviruses.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL: M10070; AAA46318.1;
CC GenBank: U00001.1;
CC InterPro: IPR001191; Gemin1_AL1.
CC Pfam: PF00759; Gemin1_AL1; 1.
CC PRINTS: PR00227; GEMCOAT1L1.
CC PROSITE: PS00228; GEMCOAT1L1.
CC ProDom: PD000736; Gemin1_AL1; 1.
CC ATP-binding. 221 228 ATP (POTENTIAL).
CC SEQUENCE 353 AA; 40130 MW; 80FA779D86029A34 CRC64;

Query Match
Best Local Similarity 58.6%; Score 215; DB 1; Length 353;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLVGEFQVDSARGSGCOTSDNAAALAAASAAALQITREKIPKYLQPHNLSNL 60
Db 110 TLVGEFQVDSARGSGCOTSDNAAALAAASAAALQITREKIPKYLQPHNLSNL 169
Oy 61 DRIFKTPPEP 70
Db 170 NRIFKTPPEP 179

RESULT 10
ID VAL1_TM0V STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DR 01-JUN-1994 (Rel. 29, Last annotation update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AL1.
OS Tomato mottle virus (Isolate Florida) (TM0V).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
Ox NCBI_TaxID=36449;
Rw SEQUENCE FROM N.A.
Rt Abouzid A.M., Polston J.E., Hiebert E.;
RA "The nucleotide sequence of tomato mottle virus, a new geminivirus
RL isolated from tomatoes in Florida.";
RT J. Gen. Virol. 73:3223-3229(1992).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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SQ SEQUENCE 359 AA; 40733 MW; 9717B4A07C93EFA7 CRC64;

DT 01-JUN-1994 (Rel. 29, Last annotation update)

Search completed: January 3, 2002, 15:57:15
Job time: 1101 sec

RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Edwards R., Eickbush D., Eickbush H., Eickbush M., Eickbush R.,
RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harless M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattell B., McInosh K.C., Meled M.P., McPherson D.,
RA Maiti S., Maiti S., Maiti S., Maiti S., Maiti S., Maiti S.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murray D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Slapson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirski K., Swirski K., Swirski K., Swirski K., Swirski K.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RA "The genome sequence of *Drosophila melanogaster*.";
RA Science 287:2185-2195(2000).

CC FUNCTION
CC MEDLINE-94230464: PubMed-8175788:
CC Kephart D., Wang B.Q., Burton Z.F., Price D.H.:
CC "Functional analysis of *Drosophila* factor 5 (TFIIF), a general
CC transcription factor.";
CC J. Biol. Chem. 269:13536-13543(1994).
CC FUNCTION: TFIIF IS A GENERAL TRANSCRIPTION INITIATION FACTOR THAT
CC PROMOTES TRANSCRIPTION OF POLYOMERIZATION OF THE TFIID
CC INITIATION COMPLEX IN COLLABORATION WITH TFIIB. IT PROMOTES
CC TRANSCRIPTION ELONGATION.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.

CC -!- SIMILARITY: TO OTHER TRANSCRIPTION FACTOR IIF, ALPHA SUBUNIT.
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CC or send an email to license@isb-sib.ch).

CC EMBL: 110931.....NOT ANNOTATED_CDS.
CC EMBL: X56982; CAA47391.....
CC EMBL: AE003675; AAF54125.1; ..
CC PIR: S30237; S30237.
CC TRANSFAC: T02173; ..
CC FlyBase: FBgn0010282; TFIIF-alpha.
CC Transcription regulation: DNA-binding; Nuclear protein.
CC FT CONFLICT 76 70 A > R (IN REF. 1).
CC FT CONFLICT 70 70 A > R (IN REF. 1).
CC FT CONFLICT 528 528 P > A (IN REF. 1).
CC SEQUENCE 577 AA: 64466 MW: 1E3DF88E3C833761 CRC64;

Query Match 19.3%; Score 69; DB 1; Length 577;
Best Local Similarity 36.4%; Pred. No. 1.8;
Matches 20; Conservative 9; Mismatches 20; Indels 6; Gaps 1;

OY 13 SARGCOTSDNDAAANAALASAAALQIIRE-----KIPKYLEQFHNLSNLD 61
DB 10 SAASCSTSAASAAAAASVASSASSSANVQEFKIRVPKPKKHVRNFATLNVD 64

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:56:24 ; Search time 131.69 seconds
(without alignments)
77.751 Million cell updates/sec

Title: US-09-289-346a-3
Perfect score: 358
Sequence: 1 TLVNGEFQVDSARGGQTF.....PQHNLSNLDIFDXKTEP 70

Scoring table:
BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Minimum Percent 100%
Listing first 45 summaries

Database : SPTREMBL17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_invertebrate.*
5: sp_human.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_protist.*
12: sp_virus.*
13: sp_unclassified.*
14: sp_unclassified.*

0920b6 tobacco lea
0950b3 tobacco lea
073572 cotton leaf
0950b3 tobacco lea
031860 okra ena1
0950b3 tobacco lea
096620 african tom
072692 beet curly
065438 beet curly
0950b3 tobacco lea
0950b3 tobacco lea
0950b3 tobacco lea
065418 beet curly
088942 tomato yell
094810 ageratum ye
091e17 cotton leaf
072723 cotton leaf
0940a7 tobacco lea
0950b3 tobacco lea
0950b3 tobacco lea
072705 cotton leaf
072719 cotton leaf
0950b3 tobacco lea
073494 okra yellow
0950b3 tobacco lea
091e17 cotton leaf

ALIGNMENTS

RESULT 1

ID 095000
DC 095000
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DE 01-JUN-2001 (TREMREL. 17, Last annotation update)
DR REPLICATION-ASSOCIATED PROTEIN.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Geminalviridae; Begonomovirus.
RN [1]_X1412-134599;
RA SEQUENCE FROM N.A.
RP Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
Zambolim E.M., Zerbini F.M.;
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
(TRMV), a Begonomovirus Isolated from Tomatoes at Triangulo Mineiro,
Rio Minas Gerais, Brazil.", the EMBL/Genbank/DBJ databases.
RT Submitted (1997-07-20), the EMBL/Genbank/DBJ databases.
DR EMBL AF291705; AGS15546.1;
DR InterPro: IP001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS: PR00227; GEMCONTAL1.
DR PRODOM: PD000736; Gemini_AL1; 1.
DR PRODOM: 352 AA; 40012 MW; 47C05583E24D613 CRC64;
SQ SEQUENCE 352 AA; 40012 MW; 47C05583E24D613 CRC64;

Query Match

Best Local Similarity 81.3%; Score 291; DB 12; Length 352;

Matches 55; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TLVNGEFQVDSARGGQTFNDAAAAAASAAALQITREKIPKYLFOFNNLSN 60

Db 11 TLVNGEFQVDSARGGQTFNDAAAAAASAAALQITREKIPKYLFOFNNLSN 170

Qy 61 DIFDXKTEP 70

Db 171 DIFDXKTEP 180

RESULT 2

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	81.3	352	12	095000
2	276	77.1	226	12	095727
3	271	75.7	314	12	092828
4	271	75.7	314	12	092828
5	264	73.7	226	12	0950b6
6	262	73.2	361	12	067574
7	260	72.6	149	12	0950b1
8	260	72.6	149	12	0950b1
9	260	72.6	233	12	0950b1
10	259	72.3	185	12	0950b1
11	251	70.1	190	12	0920b8
12	251	70.1	190	12	0920b8
13	250	69.8	190	12	0920b8
14	250	69.8	208	12	0920b8
15	250	69.8	208	12	0920b8
16	250	69.8	208	12	0920b8
17	249	69.6	208	12	0920b8
18	248	69.3	208	12	0920b8
19	247	69.0	362	12	056816

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009727
ID 009727 PRELIMINARY: PRT: 226 AA.
AC 009727;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DR 01-JUN-2001 (TrEMBLrel. 04, Last sequence update)
DE REP PROTEIN (FRAGMENT).
OS Leonurus mosalic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=58177;
RN [1]
RP SEQUENCE FROM N.A.
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
RE EMBL: U92532; AAB31157.1;
DR InterPro: IPR001191; Geminin_AL1.
DR Pfam: PF00799; Geminin_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminin_AL1; 1.
PT NOWTER 226 AA; 25617 MW; 73CDB6E765083FC5 CRC64;
SQ SEQUENCE 226 AA: 25617 MW; 73CDB6E765083FC5 CRC64;

Query Match 77.1%; Score 276; DB 12: Length 226;
Best Local Similarity 77.1%; Pred. No. 5.3e-24;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDCRSARGCGQOTNDAAALAAAGSKEAALQIIREKLPKYLQFQHNINSL 60
Db 111 TVMGEPQVDCRSARGCGQOTNDAAALAAAGSKEAALQIIREKLPKYLQFQHNINSL 170
Qy 61 DRFDKTP 70
Db 171 DRIFAKAPEP 180

009728
ID 009728 PRELIMINARY: PRT: 314 AA.
AC 009728;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DR 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE REP PROTEIN (FRAGMENT).
OS sweet potato leaf curl virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RE EMBL: AF288227; AAG01006.1;
DR InterPro: IPR001191; Geminin_AL1.
DR Pfam: PF00799; Geminin_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminin_AL1; 1.
PT NOWTER 314 AA; 35135 MW; 68622061304593F CRC64;
SQ SEQUENCE 314 AA; 35135 MW; 68622061304593F CRC64;

Query Match 75.7%; Score 271; DB 12: Length 314;
Best Local Similarity 79.4%; Pred. No. 2.9e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDCRSARGCGQOTNDAAALAAAGSKEAALQIIREKLPKYLQFQHNINSL 60
Db 111 TVMGEPQVDCRSARGCGQOTNDAAALAAAGSKEAALQIIREKLPKYLQFQHNINSL 170
Qy 61 DRFDKTP 68
Db 170 DRIFSPFP 177

009729
ID 009729 PRELIMINARY: PRT: 364 AA.
AC 009729;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DR 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE REP PROTEIN (FRAGMENT).
OS sweet potato leaf curl virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=100755;
RN [1]
RP SEQUENCE FROM N.A.
RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RE EMBL: AF104036; AAD47173.1;
DR InterPro: IPR001191; Geminin_AL1.
DR Pfam: PF00799; Geminin_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminin_AL1; 1.
PT NOWTER 364 AA; 40580 MW; 5F79752431A05D6E CRC64;
SQ SEQUENCE 364 AA; 40580 MW; 5F79752431A05D6E CRC64;

Query Match 75.7%; Score 271; DB 12: Length 364;
Best Local Similarity 79.4%; Pred. No. 3.4e-23;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDCRSARGCGQOTNDAAALAAAGSKEAALQIIREKLPKYLQFQHNINSL 60
Db 111 TVMGEPQVDCRSARGCGQOTNDAAALAAAGSKEAALQIIREKLPKYLQFQHNINSL 169
Qy 61 DRFDKTP 68
Db 170 DRIFSPFP 177

009730
ID 009730 PRELIMINARY: PRT: 226 AA.
AC 009730;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DR 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE REP PROTEIN (FRAGMENT).
OS tomato mild mottle geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
NCBI_TaxID=92943;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakhla M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RE EMBL: AF131071; AAD33471.1;
DR InterPro: IPR001191; Geminin_AL1.
DR Pfam: PF00799; Geminin_AL1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminin_AL1; 1.
PT NOWTER 226
SQ SEQUENCE 226

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[illegible]


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RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001318; BAA34039.1; -.
DR InterPro: IPR001191; Gemini-AL1.
DR RefSeq: NC_000736; Gemini-AL1.
DR PRINTS: PR00727; GEMCOATALL.
DR ProDom: PD000736; Gemini-AL1; 1.
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FT NON_TER 1 190
SQ SEQUENCE 190 AA: 21444 MW: AAC12943E3F01AD CRC64:

Query Match 70.18; Score 251; DB 12; Length 190;
Best Local Similarity 58.88; Pred. No. 3.3e-21;
Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVWGFQVQDSARGCGCTSDNAAAALAASSAAALQIIREKIPKYLQFPHNLSNL 60
Db 85 TLWNGFTQDSARGCGCNQKACALNAKASAKALAIIREKLPKDFIYHNLNSL 144
Oy 61 DRI-----FUKTPE 69
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Db 145 DRIAPPLEVFVCPFSNSSFQDQVE 169

RESULT 13
ID Q94827 PRELIMINARY; PRT; 190 AA.
AC Q94827.
EN 1 TLVWGFQVQDSARGCGCTSDNAAAALAASSAAALQIIREKIPKYLQFPHNLSNL 60
RC STRAIN=GORAL1;
RT Ool K., Ohshita S., Ishii I., Yahara T.;
RA "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001264; BAA33992.1; -.
DR RefSeq: NC_000736; Gemini-AL1.
DR PRINTS: PR00759; Gemini-AL1.
DR ProDom: PD000736; Gemini-AL1; 1.
FT NON_TER 1 190
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SQ SEQUENCE 190 AA: 21444 MW: 93C742A8EBDB7EB CRC64:

Query Match 69.88; Score 250; DB 12; Length 190;
Best Local Similarity 58.88; Pred. No. 4.3e-21;
Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVWGFQVQDSARGCGCTSDNAAAALAASSAAALQIIREKIPKYLQFPHNLSNL 60
Db 85 TLWNGFTQDSARGCGCNQKACALNAKASAKALAIIREKLPKDFIYHNLNSL 144
Oy 61 DRI-----FUKTPE 69
|||
|||
Db 145 DRIAPPLEVFVCPFSNSSFQDQVE 169

RESULT 14
ID Q920C4 PRELIMINARY; PRT; 208 AA.
AC Q920C4.
EN 1 TLVWGFQVQDSARGCGCTSDNAAAALAASSAAALQIIREKIPKYLQFPHNLSNL 60
RC STRAIN=ABURA3;
RT Ool K., Ohshita S., Ishii I., Yahara T.;
RA "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001264; BAA33992.1; -.
DR RefSeq: NC_000736; Gemini-AL1.
DR PRINTS: PR00759; Gemini-AL1.
DR ProDom: PD000736; Gemini-AL1; 1.
FT NON_TER 1 208
FT NON_TER 1 208
SQ SEQUENCE 208 AA: 23486 MW: E301135F799C3DAD CRC64:

Query Match 69.88; Score 250; DB 12; Length 208;
Best Local Similarity 58.88; Pred. No. 4.8e-21;
Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVWGFQVQDSARGCGCTSDNAAAALAASSAAALQIIREKIPKYLQFPHNLSNL 60
Db 102 TLWNGFTQDSARGCGCNQKACALNAKASAKALAIIREKLPKDFIYHNLNSL 161
Oy 61 DRI-----FUKTPE 69
|||
|||
Db 162 DRIAPPLEVFVCPFSNSSFQDQVE 186

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Search completed: January 3, 2002, 15:56:24
Job time: 1120 sec

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT INVENTION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-8

Query Match 60.98; Score 218; DB 4; Length 361;
Best Local Similarity 57.18; Pred. No. 2.4e-21;
Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLVWCFQVDCRSARGCQTSNDAAALAAASSAAALQIIRKIPKYLFOHNNISNL 60
DB 110 TLWGQFQVDCRSARGCQTSNDAAALAAASSAAALQIIRKIPKYLFOHNNISNL 169

OY 61 DRIEDKTEP 70
DB 170 ERIEAKPEP 179

RESULT 5
US-08-838-151A-44
; Sequence 44, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Juu, Hany Douglas
; APPLICANT: Alquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pressler, Reckey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-44

Query Match 60.98; Score 217; DB 4; Length 353;
Best Local Similarity 58.68; Pred. No. 3.2e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLVWCFQVDCRSARGCQTSNDAAALAAASSAAALQIIRKIPKYLFOHNNISNL 60
DB 110 TLWGQFQVDCRSARGCQTSNDAAALAAASSAAALQIIRKIPKYLFOHNNISNL 169

OY 61 DRIEDKTEP 70
DB 170 ERIEAKPEP 179

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Juu, Hany Douglas
; APPLICANT: Alquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pressler, Reckey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 60.98; Score 217; DB 4; Length 353;
Best Local Similarity 58.68; Pred. No. 3.2e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLVWCFQVDCRSARGCQTSNDAAALAAASSAAALQIIRKIPKYLFOHNNISNL 60
DB 110 TLWGQFQVDCRSARGCQTSNDAAALAAASSAAALQIIRKIPKYLFOHNNISNL 169

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OY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

RESULT 7

US-08-838-151A-49
: Sequence 49, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: CORRESPONDENCE ADDRESS: Rockey, Minamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTY/REGISTRATION INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION NO: 49:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 353 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 60.6%; Score 217; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 3.2e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLVWGFEVDGRSGRGCGTNSDAAAALQIIREKTPKYLQFPHNLSNL 60
DB 110 TLVWGFEVDGRSGRGCGQSANSTAKALNADSTESAITLKEQPDYVLQHHNLSNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

RESULT 8

US-08-838-151A-52
: Sequence 52, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul

: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: CORRESPONDENCE ADDRESS: Rockey, Minamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTY/REGISTRATION INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 353 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-52

Query Match 60.6%; Score 217; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 3.2e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLVWGFEVDGRSGRGCGTNSDAAAALQIIREKTPKYLQFPHNLSNL 60
DB 110 TLVWGFEVDGRSGRGCGQSANSTAKALNADSTESAITLKEQPDYVLQHHNLSNL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

RESULT 9

US-08-838-151A-55
: Sequence 55, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: CORRESPONDENCE ADDRESS: Rockey, Minamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/638,151A
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-638-151A-55

Query Match 60.6%; Score 217; DB 4; Length 353;
Best Local Similarity 58.5%; Pred. No. 3.2e-21;
Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0:
QY 1 TLWGCFQVDSRGSGCQTSDNRAAALAAASAAALQIIRKTPKYLFPFHLSNLD 60
DB 110 TIENGQFVDSRGSGCQTSDNRAAALAAASAAALQIIRKTPKYLFPFHLSNLD 169
QY 61 DRFDKTPPEP 70
DB 170 ERIFVKVPEP 179

RESULT 10
US-08-809-103B-2
Sequence 2, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
CLASSIFICATION: 800
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 521-0573
TELEX: 248425 EMBON

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 59.2%; Score 212; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0:
QY 2 LVNGCFQVDSRGSGCQTSDNRAAALAAASAAALQIIRKTPKYLFPFHLSNLD 61
DB 111 LVNGTFQVDSRGSGCQTSDNRAAALAAASAAALQIIRKTPKYLFPFHLSNLD 170
QY 62 RIFDKTPPEP 70
DB 171 KVFQVPPAP 179

RESULT 11
US-08-809-103B-4
Sequence 4, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
CLASSIFICATION: 800
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 59.2%; Score 212; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 1.5e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0:

```

: Sequence 9, Application US/08809103B
: Patent No. 6133505
: GENERAL INFORMATION:
: APPLICANT: GRONENBORN, Bruno
: TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
: TO TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
: NUMBER OF SEQUENCES: 17
: COMPLETION DATE: 17-SEP-1995
: ADDRESSER: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: NAME: PATENT INFORMATION SYSTEM
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/809,103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: D00
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J
: ADDRESS: 32, 925
: STREET: 32nd Street, N.W.
: REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: TELEX: 248425 EMBON
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1738 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-809-103B-8
:
: Query Match 59.38; Score 212; DB 4; Length 359;
: Pair Local Similarity 56.58; Protein 1, 5-20;
: Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
:
: QY 2 LVWGFEVDGSRGSGGCGTNDAAAAAALAAASAAALQIREKIPKYLFGFHNLSNLD 61
: DB 111 LNWGTFDGRSGGGQGTANDYAKAINAGSKAQDVLKELAPRYYLHFHINTNSLD 170
:
: QY 62 RIFDKTEPP 70
: DB 171 KVFQVFPAP 179
:
: RESULT 14
: US-08-838-151A-20
: Sequence 20, Application US/08838151A
: Patent No. 6133505
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
: COMPLETION DATE: 17-SEP-1995
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:

```

RESULT.	14
US-08-638-151A-20	
: Sequence 20, Application US/08838151A	
: Patent No. 6291743	
: GENERAL INFORMATION:	
: APPLICANT: Stout, John T	
: APPLICANT: Luu, Hang T	
: APPLICANT: Maxwell, Douglas	
: APPLICANT: Ahlquist, Paul	
: APPLICANT: Hanson, Steve	
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus	
: NUMBER OF INVENTION: 63	
: CORRESPONDENCE ADDRESS:	

ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 20:
 LENGTH: 357 amino acids
 TYPE: amino acid
 MOLECULE TYPE: linear
 US-08-838-151A-20

Query Match 53.1% Score 190; DB 4; Length 357;
 Best Local Similarity 60.7%; Pred. No. 1.4e-17;
 Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Oy 4 WGFQVGHSGRGCGTSDNDRAAALAAASSAAALQIIPKIPKXYLQFHNLSNLDRI 63
 Db 111 FGVQIDGSRGCGQGSANDAYAEALNSGSKSEALNLKPKDYILOFHNLSNLDRI 170
 Oy 64 F 64
 Db 171 F 171

RESULT 15
 US-08-838-151A-24
 : Sequence 24, Application US/08038151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Scout, John T
 : INVENTOR: Scout, John T
 : APPLICANT: Alquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS: Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/838,151A
 : FILING DATE:
 : CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 24:
 LENGTH: 357 amino acids
 TYPE: amino acid
 MOLECULE TYPE: linear
 US-08-838-151A-24

Query Match 53.1% Score 190; DB 4; Length 357;
 Best Local Similarity 60.7%; Pred. No. 1.4e-17;
 Matches 37; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Oy 4 WGFQVGHSGRGCGTSDNDRAAALAAASSAAALQIIPKIPKXYLQFHNLSNLDRI 63
 Db 111 FGVQIDGSRGCGQGSANDAYAEALNSGSKSEALNLKPKDYILOFHNLSNLDRI 170
 Oy 64 F 64
 Db 171 F 171

Search completed: January 3, 2002, 15:38:49
 Job time: 226 sec


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:      January 3, 2002, 15:37:36 ; Search time 144.17 Seconds
              (without alignments)
              35.965 Million cell updates/sec

Title:       US-09-289-346A-4
Perf score:   361
Sequence:     1 TLWGFQFQVDSRGSGCOT.....FQFHNSLNDRFDKPTPEP 70

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Scoring table: BLOSUM62
Gapop 10.0, Gapext: 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2:	/SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
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6:	/SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
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9:	/SID58/gcgdata/geneseq/geneseq/AA1988.DAT.*
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19:	/SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
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21:	/SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
1	361	100.0	70	21	AAB18680	Mutant peptide der	
2	346	95.8	70	21	AAB18677	Amino acid sequenc	
3	348	95.6	306	11	AAB18685	Mutant peptide der	
4	338	93.6	70	21	AAB18685	Mutant peptide der	
5	335	92.8	70	21	AAB18688	Mutant peptide der	
6	334	92.5	70	21	AAB18692	Mutant peptide der	
7	332	92.0	70	21	AAB18684	Mutant peptide der	
8	332	92.0	70	21	AAB18690	Mutant peptide der	
9	331	91.7	70	21	AAB18686	Mutant peptide der	
10	330	91.4	70	21	AAB18689	Mutant peptide der	
11	331	91.4	70	21	AAB18686	Mutant peptide der	

Mutant peptide der
Mutant peptide der
Mutant peptide der
Mutant peptide der
Sardinian tomato y
Sardinian tomato y
Bean golden mosaic
Bean golden mosaic
Bean golden mosaic
Bork 4 gene product
Tomato mottle virus
Tomato mottle virus
Tomato mottle virus
Product of ORF 6
Tomato yellow leafy
Tomato yellow leafy
Tobacco leaf curl vi
HIV-1 strain YN303
Arabidopsis thaliana
Hyphorin ORF 22ase
Candida albicans C
Amino acid sequenc
C glutamicum proteas
Tomato mottle virus
Mimic acid sequenc
Mimic acid sequenc
Protein M1 encoded

ALIGNMENTS

[illegible]

PT	comprise a nucleic acid construct containing a nucleic acid sequence
PT	encoding a mutant A11 protein with a mutation in the Rb binding region
PT	
XX	Claim 53; Page 46; 73pp; English.
CC	The present sequence represents a mutant peptide, derived from a
CC	geminivirus replication (Rep) protein, also known as A11. A11 binds
CC	double-stranded DNA, with cleavage and ligation of single-stranded
CC	DNA. A11 is a transgenic plant. A11 is a mutant A11 protein. A11
CC	protein are used to produce transgenic plants. The mutation in A11 is
CC	present in a ribosome binding region, and expression of mutant A11
CC	protein imparts increased resistance to geminivirus infection in the
CC	plant. Mutant A11 proteins are useful for producing plants having
CC	increased resistance or reduced sensitivity to a geminivirus such as
CC	tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC	virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC	virus, cotton leaf curl virus or beet curly top virus.
CC	
XX	Sequence 70 AA:
SO	

Query Match	93.5%	Score 338	DB 21	Length 70
Best Local Similarity	94.3%	Pred. No. 8e-37	4	Indels 0
Matches 66	Conservative 0	Mismatches 0	Caps 0	
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QY	1	TLVNGEPOVDGRSGRGCTSDNDAAEALNASKKEELQITAAAIPEKYLQFHNINSL	60	
Db	1	tlvgeitqvgdsarggcqtsndaaealnaskkeelqirektpakylqfhninsl	60	
QY	61	DRIFDKTPEP 70		
Db	61	drifdktppep 70		
<hr/>				
RESULT	5			
AAAB18688				
ID	AAAB18688	standard: peptide: 70 AA.		
XX	AAAB18688:			
XX				
DT	22-JAN-2001	(first entry)		
DE	XX			
DE	XX	Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.		
XX	XX	Geminivirus; replication protein; Rep protein; ALI; transgenic plant;		
KW	XX	ribosome binding region; resistance: geminivirus infection.		
XX	XX			
XX	XX	Synthetic.		
XX	XX	Tomato golden mosaic virus.		
XX	XX			
Key	XX	Location/Qualifiers		
PH	FT	Misc-difference 19		
FT	FT	/note= "wild type residue replaced with Ala"		
FT	FT	Misc-difference 20		
FT	FT	/note= "wild type residue replaced with Ala"		
XX	XX	WC2000054573-AL.		
XX	XX	21-SEP-2000.		
PD	XX			
PF	XX	15-MAR-2000; 2000UC0506759.		
XX	XX			
XX	XX	18-MAR-1999; 99US-0125004.		
PR	XX	09-APR-1999; 99US-0289346.		
XX	XX	(UYNC-) UNIV NORTH CAROLINA STATE.		
XX	XX			
PI	XX	Hanley-Bowdoin L, Orozco BW, Kong L;		
DR	WPI:	2000-618#51/59		

PT Transgenic plants with increased resistance to geminivirus infection

Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region.

Disclosure: Page 48; 73pp: English.

The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a region of the protein that is essential for the A11 protein to impart increased resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA:

Query Match 92.8%; Score 335; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 2e-36; 5; Indels 0; Gaps 0;
 Matches 65; Conservative 0; Mismatches 5;

OY 1 TLVWGFEVDGRSGAGCGCTSDNDAAEALNASKEEALQITAAALPEKYLQFPHINSNL 60
 DB 1 TLVWGFEVDGRSGAGCGCTSDNDAAEALNASKEEALQITAAALPEKYLQFPHINSNL 60
 OY 61 DRIFDKTPPP 70
 DB 61 DRIFDKTPPP 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide: 70 AA.
 AC AAB18692;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 PN 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UWNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;

WPI: 2000-618851/59.

Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region.

Disclosure: Page 50; 73pp: English.

The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a region of the protein that is essential for the A11 protein to impart increased resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA:

Query Match 92.5%; Score 334; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 2.7e-36;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLVWGFEVDGRSGAGCGCTSDNDAAEALNASKEEALQITAAALPEKYLQFPHINSNL 60
 DB 1 TLVWGFEVDGRSGAGCGCTSDNDAAEALNASKEEALQITAAALPEKYLQFPHINSNL 60
 OY 61 DRIFDKTPPP 70
 DB 61 DRIFDKTPPP 70

RESULT 7
 AAB18684
 ID AAB18684 standard; peptide: 70 AA.
 AC AAB18684;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 PN 21-SEP-2000.
 PD 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UWNC-) UNIV NORTH CAROLINA STATE.

XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the Rb binding region
XX
XX
XX Claim 52; Page 45; 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as A11. A11 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the A11
XX protein are used to produce transgenic plants. The mutation in A11 is
XX present in a ribosome binding region, and expression of mutant A11
XX protein imparts increased resistance to geminivirus infection in the
XX transgenic plants. The mutation in A11 is located in the A11 protein
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant A11 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:

Query Match 92.0% Score 332; DB 21; Length 70;
Best Local Similarity 92.9% Pred. No. 4.9e-36;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TLVGEFQVDCRSARGSCOTSDNDAAAEALNASSKEEALQIIAAAIPEKYLQPHNLSNL 50

Db 1 TLVGEAAVGRSARGSCQTSNDAAAEALNASSKEEALQIIIREKIPKYLQPHNLSNL 50

Oy 61 DRIFDKTPEP 70

Db 61 drifdktp 70

RESULT 8
AAB18690
ID AAB18690 standard; peptide: 70 AA.

AC AAB18690;

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX
XX Geminivirus; replication protein; Rep protein; A11; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

XX Misc-difference 27 /note= "wild type residue replaced with Ala"

XX Misc-difference 30 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the Rb binding region
XX
XX
XX Disclosure; Page 49; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as A11. A11 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the A11
XX protein are used to produce transgenic plants. The mutation in A11 is
XX present in a ribosome binding region, and expression of mutant A11
XX protein imparts increased resistance to geminivirus infection in the
XX transgenic plants. The mutation in A11 is located in the A11 protein
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant A11 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:

Query Match 92.0% Score 332; DB 21; Length 70;
Best Local Similarity 92.9% Pred. No. 4.9e-36;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 TLVGEFQVDCRSARGSCOTSDNDAAAEALNASSKEEALQIIAAAIPEKYLQPHNLSNL 50

Db 1 TLVGEAAVGRSARGSCQTSNDAAAEALNASSKEEALQIIIREKIPKYLQPHNLSNL 50

Oy 61 DRIFDKTPEP 70

Db 61 drifdktp 70

RESULT 9
AAB18678
ID AAB18678 standard; peptide: 70 AA.

AC AAB18678;

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX
XX Geminivirus; replication protein; Rep protein; A11; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

XX Misc-difference 12 /note= "wild type residue replaced with Ala"

XX Misc-difference 13 /note= "wild type residue replaced with Ala"

XX Misc-difference 15 /note= "wild type residue replaced with Ala"

XX WO200054573-A1.

XX 21-SEP-2000.


```

FT XX /note= "wild type residue replaced with Ala"
FT XX W02000054573-A1.
FT XX
FT XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000: 2000WO-US06759.
XX
XX 18-MAR-1999: 99US-0125004.
PR
XX 09-APR-1999: 99US-0249346.
PR
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the RB binding region
XX .
XX
XX Disclosure: Page 48-49: 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as A11. A11 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA and interacts with other viral and host proteins. Mutants of the A11
XX protein are used to produce transgenic plants. The mutation in A11 is
XX present in a ribosome binding region, and expression of mutant A11
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant A11 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:
XX
XX Query Match 91.4%; Score 310; DB 21: Length 70;
XX Best Local Similarity 92.9%; Pred. No. 8.9e-36;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 TLWGFVFGVGRSGCGTSSNDAAEALNASSKEALQIIAAIPKYLQFHNLNSL 60
XX Db 1 TLWGFVFGVGRSGCGTSSNDAAEALNASSKEALQIIAAIPKYLQFHNLNSL 60
XX
XX QY 61 DRFDKTPPEP 70
XX Db 61 drfdktpep 70
XX
XX RESULT 12
XX AAB18691 standard; peptide: 70 AA.
XX
XX AC AAB18691;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX
XX DE Geminivirus: replication protein; Rep protein: A11; transgenic plant;
XX
XX KW ribosome binding region: resistance; geminivirus infection.
XX
XX OS Synthetic.
XX
XX OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 34

```

```

FT XX /note= "wild type residue replaced with Ala"
FT XX W02000054573-A1.
FT XX
FT XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000: 2000WO-US06759.
XX
XX 18-MAR-1999: 99US-0125004.
PR
XX 09-APR-1999: 99US-0249346.
PR
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the RB binding region
XX .
XX
XX Disclosure: Page 48-49: 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as A11. A11 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA and interacts with other viral and host proteins. Mutants of the A11
XX protein are used to produce transgenic plants. The mutation in A11 is
XX present in a ribosome binding region, and expression of mutant A11
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant A11 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:
XX
XX Query Match 90.9%; Score 328; DB 21: Length 70;
XX Best Local Similarity 91.4%; Pred. No. 1.6e-35;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 TLWGFVFGVGRSGCGTSSNDAAEALNASSKEALQIIAAIPKYLQFHNLNSL 60
XX Db 1 TLWGFVFGVGRSGCGTSSNDAAEALNASSKEALQIIRKPKYLQFHNLNSL 60
XX
XX QY 61 DRFDKTPPEP 70
XX Db 61 drfdktpep 70
XX
XX RESULT 13
XX AAB18691 standard; peptide: 70 AA.
XX
XX AC AAB18691;
XX
XX DT 22-JAN-2001 (first entry)
XX
XX DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX
XX DE Geminivirus: replication protein; Rep protein: A11; transgenic plant;
XX
XX KW ribosome binding region: resistance; geminivirus infection.
XX
XX OS Synthetic.
XX
XX OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 35

```

OS XX Tomato golden mosaic virus.

FH XX Key Location/Qualifiers

FT XX Misc-difference 47 /note= "wild type residue replaced with Ala"

FT XX Misc-difference /note= "wild type residue replaced with Ala"

FT XX Misc-difference 49 /note= "wild type residue replaced with Ala"

FT XX Misc-difference /note= "wild type residue replaced with Ala"

PN XX WO200054573-A1.

XX XX 21-SEP-2000.

XX XX 15-MAR-2000; 2000WO-US06759.

PR XX 18-MAR-1999; 99US-0125004.

PR XX 09-APR-1999; 99US-0289346.

PA XX (UYNC-) UNIV NORTH CAROLINA STATE.

PT XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX XX WPI: 2000-618851/59.

XX XX Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region.

PT XX

PS XX Claim 52: Page 44; 73pp: English.

XX XX The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a ribosome binding region, and expression of mutant A11 protein imparts resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

XX XX Sequence 70 AA:

Query Match 90.0%; Score 325; DB 21: Length 70;
Best Local Similarity 91.4%; Pred. NO. 5.4e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TLWGEFQVDRAGGCCTSDNAAEAALNASSKEAQLQITAAAIPEKYLQPHNLSNI 60

Db 1 tlwgefqvdraggcctandaaeaalnasseeaqlireklpaaalfqfhnlsnll 60

OY 61 DRIFDKTPEP 70

Db 61 drifdktp 70

RESULT 14

ID AAB18683

XX AAB18683 standard; peptide: 70 AA.

XX AAB18683;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX

KW XX Geminivirus: replication protein; Rep protein; A11; transgenic plant; ribosome binding region; resistance; geminivirus infection.

XX XX Synthetic.

OS XX Tomato golden mosaic virus.

FH XX Key Location/Qualifiers

FT XX Misc-difference 59 /note= "wild type residue replaced with Ala"

FT XX Misc-difference 61 /note= "wild type residue replaced with Ala"

FT XX Misc-difference 62 /note= "wild type residue replaced with Ala"

PN XX WO200054573-A1.

XX XX 21-SEP-2000.

XX XX 15-MAR-2000; 2000WO-US06759.

PR XX 18-MAR-1999; 99US-0125004.

PR XX 09-APR-1999; 99US-0289346.

PA XX (UYNC-) UNIV NORTH CAROLINA STATE.

PT XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX XX WPI: 2000-618851/59.

XX XX Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region.

PT XX

PS XX Claim 53: Page 45; 73pp: English.

XX XX The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a ribosome binding region, and expression of mutant A11 protein imparts increased resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

XX XX Sequence 70 AA:

Query Match 89.8%; Score 324; DB 21: Length 70;
Best Local Similarity 91.4%; Pred. NO. 5.4e-35;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TLWGEFQVDRAGGCCTSDNAAEAALNASSKEAQLQITAAAIPEKYLQPHNLSNI 60

Db 1 tlwgefqvdraggcctandaaeaalnasseeaqlireklpaaalfqfhnlsnll 60

OY 61 DRIFDKTPEP 70

Db 61 aaifdktp 70

RESULT 15

ID AAB18682

XX AAB18682 standard; peptide: 70 AA.

XX AAB18682;

XX

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:08 ; Search time 72.79 seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346A-4

Perfect score:

Sequence: 1 TLVWGEFQVDGRSARGCQT.....FOFHNLSNLDRIFDKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : PTP 68-4

```

outchouse ,
      1:  plr1:*
      2:  plr2:*
      3:  plr3:*
      4:  plr4:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query No.	Score	% Match	Length	DB	ID	Description
1	346	95.8	352	1	QOCVLI		All protein - toma
2	249	69.0	361	1	QOCVPT		All protein - pota
3	240	66.5	358	2	S07594		hypothetical prote
4	233	64.5	362	1	Q01887		All protein - toma
5	222	61.5	349	2	Q02400		gene C1 protein
6	222	61.5	349	2	Q02400		gene C1 protein
7	222	61.5	349	2	S31875		All protein - pepp
8	222	61.5	359	2	S32593		hypothetical prote
9	219	60.7	359	2	S39235		gene C1 protein -
10	216	59.8	351	2	Q02327		All protein - indi
11	216	59.8	355	1	QOCVMI		AVI protein - abut
12	210	58.3	355	2	S28390		All protein - beet
13	210	58.3	355	2	S28390		All protein - toma
14	200	55.4	357	1	QOCVCI		All protein - toma
15	199	55.1	360	2	S59885		replication-associ
16	134	37.1	131	2	S45059		ACI protein (clone
17	128	35.5	347	1	QOCVSI		All protein - squa
18	72	19.6	587	2	JC1419		Fe gamma (170) rec
19	63.5	17.5	584	2	T19061		hypothetical prote
20	61.5	17.0	584	2	T19061		hypothetical prote
21	61.5	17.0	584	2	T19061		hypothetical prote
22	61.5	17.0	584	2	T19061		hypothetical prote
23	61.5	17.0	584	2	T19061		hypothetical prote
24	61.5	17.0	584	2	T19061		hypothetical prote
25	61.5	17.0	584	2	T19061		hypothetical prote
26	61.5	17.0	584	2	T19061		hypothetical prote
27	61.5	17.0	584	2	T19061		hypothetical prote
28	60.5	16.8	159	2	S64077		NADH dehydrogenase
29	60	16.6	767	2	F71379		hypothetical prote

ALIGNMENTS

RESULT 1
QCCVLI
A:1 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
C:Name: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text_change 08-Apr-1994
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Restructures: 1-352 <RAN>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A and DNA B.
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

	Query Match	95.8%	Score 346	DB 1	Length 352
	Best Local Similarity	95.7%	Pred. No. 3e-33		
	Matches	67	Conservative	0	Mismatches
				3	Indels
				0	Gaps
Qy	1	TLVWGEPQVDSARGSGCQTSDNDAAEALNASKEEALQIIAAATPKYLFQFHNLNSNL	60		
D6	111	TLVWGEPQVDSARGSGCQTSDNDAAEALNASKEEALQIIIREKTPKYLQFHNLNSNL	170		
Qy	61	DRFQKTPPEP 70			
D6	171	DRFQKTPPEP 180			

RESULT 2

QCVPT

ALI protein - potato yellow mosaic virus (isolate Venezuela)

C-Specific 30-1992

Sequence_revision 30-Jun-1992

text_change 16-Jun-2000

Accession J00364

KeyWords: R.H.A.; Coffin R.S.; Roberts E.J.F.; Hamilton, W.D.O.

A:Title: The nucleotide sequence of the infectious cloned DNA components of potato Y virus
A:Reference number: J00362; MUID:91311403
A:Accession: J00362
A:Accession number: not shown
A:Molecule type: DNA
A:Residues: 1-361 <CU>
A:Cross-references: GB:000940; NID:g222458; PID:BAA00782.1; PID:g222459
C:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

```

Query Match      69.0%; Score 249; DB 1; Length 361;
Best Local Similarity 68.1%; Pred. No. 9.4e-22;
Matches 43; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Oy 1 TLWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLENGEFOIDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 169
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 DRIFDKTPEP 69
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRIFDKTPEP 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C:Accession: S39211; E.: Accotto, G.; Moriones, E.
C:Reference: Genbank: AF048362
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174930
A:Accession: S07594
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-359 <NDR>
A:Cross-references: EMBL:X17095; NID:g59371; PIDN:CAA34953.1; PID:g59376
C:Genetics:
C:Map position: segment DNA1
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match      66.5%; Score 240; DB 2; Length 358;
Best Local Similarity 64.4%; Pred. No. 1.2e-20;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Oy 1 TLWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 TVWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 168
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 DRIFDKTPEP 70
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 DRIFDKTPEP 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
JQ1887
A:Title: Complete nucleotide sequence of pepper huasteco virus (strain Australia)
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
C:Accession: JQ1887
R:Dr. J.B.; Rigden, J.E.; Krake, L.R.; Mullineaux, P.N.; Rezaian, M.A.
J. Gen. Virol. 74, 147-151, 1993
A:Reference number: JQ1885; MUID:9313978
A:Accession: JQ1887
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match      64.5%; Score 233; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 7.4e-20;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

Oy 1 TLWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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Db 110 TLENGEFOIDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 169
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 DRIFDKTPEP 69
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRIFDKTPEP 194
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
gene C1 protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S39211; E.: Accotto, G.; Moriones, E.
C:Reference: Genbank: AF048362
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S39209
A:Accession: S39211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <NDR>
A:Cross-references: EMBL:X17095; NID:g433655; PIDN:CAA81026.1; PID:g433658
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match      63.4%; Score 229; DB 2; Length 359;
Best Local Similarity 60.9%; Pred. No. 2.2e-19;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LNWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 LEMGTFOIDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 170
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 62 DRIFDKTPEP 70
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 DRIFDKTPEP 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
JQ2300
replicase - pepper huasteco virus (component A)
N:Alternate names: ORF ALL protein
C:Species: pepper huasteco virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999
C:Accession: JQ2300
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estralla, L.; Rivera-Bustamante,
J. Gen. Virol. 74, 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b
A:Reference number: JQ2259; MUID:94015007
A:Accession: JQ2300
A:Molecule type: DNA
A:Residues: 1-490 <DRY>
A:Cross-references: GB:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match      61.5%; Score 222; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 1.4e-18;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Oy 1 TLWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TVWGEFQDGRSARGGCGTSDNDAAEALNASKEEALQITAAAIPEKYLFOFHNLNSL 169
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Oy 61 DRIFDKTPEP 70
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRIFDKTPEP 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S31875
A:Title: Complete nucleotide sequence of pepper huasteco virus
C:Species: pepper huasteco virus

```

C-Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
C-Accession: S22593
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-Buonafina, P. et al. 1999. The complete nucleotide sequence of pepper huasteco virus: analysis and comparison with other tobamoviruses. *Arch. Virol.* 144: 107-117.
A-Description: Complete nucleotide sequence of pepper huasteco virus: analysis and comparison with other tobamoviruses. *Arch. Virol.* 144: 107-117.
A-Reference number: S21872
A-Accession: S21875
A-Title: Tobacco yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite virus.
A-Molecule type: DNA
A-Residues: 1-349 <TOR>
A-Cross-references: EMBL:X70418; NID:g61023; PIDN:CAA49856.1; PID:g61025
A-Note: the source is designated as pepper huasteco virus
C-Superfamily: tomato golden mosaic virus All protein

Query Match 61.5% Score 222; DB 2; Length 349;
Best Local Similarity 60.0%; Prd No. 1; 4e-18;
Matches 42; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 1 TLVKGFEVQDGSARGCGTSTNDAAAFANLNASKEALQITAAATPKYLFQPHLNSNL 60
I: |||||:|||||||: || |||||:|||||||: |||||: |||||: |||||: |||||: ||
Db 110 TVMGFEVQDGSARGCGQSANTYAKALNSASAEALQIIRKPEQPHFLQPHNVSNA 169
QY 61 DSTKPTPEP 70
I: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
Db 170 NRIFQTPPEP 179

RESULT 8
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C-Species: tomato yellow leaf curl virus
C-Accession: S22593 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
C-Title: Tobacco yellow leaf curl virus
R-Keyw-Four: A.; Bendahmane, M.; Watzeit, V.; Accotto, G.P.; Crespi, S.; Gromeborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A-Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite virus.
A-Reference number: S22588; NUID:92107660
A-Accession: S22593
A-Status: preliminary; nucleic acid sequence not shown; translation not shown
A-Molecule type: DNA
A-Residues: 1-349 <TOR>
A-Cross-references: EMBL:X61153; NID:g62211; PIDN:CAA43466.1; PID:g62217
A-Note: the nucleotide sequence was submitted to the EMBL data library, August 1991
C-Superfamily: tomato golden mosaic virus All protein

```

Query Match          51.5%;   Score 222;   DA 2;   Length 359;
Best Local Similarity 58.0%;   Pred. 0.15e-18;
Matches 40;   Conservative 10;   Mismatches 19;   Indels 0;   Gaps 0;

QY      2  LWGEPQVDSRGAGCGQTNDAAEALNASKKEALQITAAAPKPYLFQFHNLSND 61
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      111  LKNGTFQIDDSNGSGQQTNDAYANALNASKSADLVKELAPRYVLFHFNLSND 170

QY      67  RFDKTPPEP 70
      :||  ||
Db      171  KVFQPPAP 179

RESULT      9
gene C1 protein - tomato yellow leaf curl virus
S39235
C:Species: tomato yellow leaf curl virus
C:Accession: S39235
C:Accession: S39235
R:Crespi, S.; Noris, A.; Bosco, D.; Accotto, G.
submitted to the EMBL Data Library, December 1993
A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity
A:Reference number: S39233
A:Accession: S39235
A:Accession: S39235
A:Accession: S39235
A:Molecule type: DNA

```

```

A:Residues: 1-359 <CRE>
A:Cross-references: EMBL: Z28390; NID: g1041571; PID: g1334964
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 60.7% Score 219; DB 2; Length 359;
      Blast Local Similarity 38.0%; Pred. No. 3,3e-19;
      Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IVGSEFVGWGRSGGCGTNDAAAEALNASSKEEAQIIATAAIPKYLFPFNLNSNLD 61
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 LEMGTFQIDNSRGSGQGTANDAYAKAINASSKSEALDIQLAPRDYVLRHFNISNLD 170

QY 62 RIPTKTPPP 70
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 KVFQVPAP 179

RESULT 10
JQ2327
AL1 protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Date: 28-Aug-1985
C:Accession: JQ2327; S35983
R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-t
A:Reference number: JQ2326; MDID: 94065670
A:Accession: JQ2327
A:Molecule type: DNA
C:Superfamily: EMBL: Z24756; NID: g395351; PIDN: CAA80891.1; PID: g584046
C:Superfamily: tomato golden mosaic virus AL1 protein

```

```

Query Match          59.8%; Score 216; DB.2: Length 351;
Best Local Similarity 61.2%; Pref. No. 7,3e-18;
Matches 41: Conservative 0; Gaps 0; Mismatches 17; Indels 0;

QY      4  WGEFVDSRGSGCCCTGNDAAAEALNASSEKAQLIIRAAIPKYLQFNHLSNIDRI 63
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     113  WTGFQDLSRAGCGGSANDYAALNLNGSKSGLKILNELAPDYLRDFHLSSLNIDRI 172
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      64  FDKTPEP 70
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     173  FTKPPPP 179
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
OCQWV1
AVI protein - abutilon mosaic virus (isolate west India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
C:Accession: A36214
RefScimuth, T.; Zimmatt, G.; Jeske, H.
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as
A:Reference number: A36214; MUID:91020984
A:Accession: A36214
A:Molecule type: DNA
A:Residues: 1-355 <PRI>
A:CROSS-References: EMBL:X15993
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus All protein

```

Query Match 59.9%; Score 216; DB 1; Length 355;
Best Local Similarity 58.5%; Pred. No. 7,4e-18;
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
OV 1 TLWKEFQDGRSGRGCTSDNDAAEANASKSFEALQITAAATPEKYLFQPHNLNSNI 60

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: January 3, 2002, 15:57:15 : Search time 43.68 Seconds
(without alignments)
58.758 Million cell updates/sec

Title: US-09-289-346a-4

Perfect score: 361

Sequence: 1 TLVWGEFQVDSARGCCT.....EQFHNLNSLDRIFDKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	95.8	352	1 VAL1_TGMV	P03567 tomato yell
2	249	69.0	361	1 VAL1_PTMV	P27258 potato yell
3	240	66.5	361	1 VAL1_PTMV	P27258 potato yell
4	240	66.5	361	1 VAL1_PTMV	P27258 potato yell
5	233	64.5	362	1 VAL1_TYIC	P14972 cassava lat
6	229	63.4	359	1 VAL1_TYIC	P36279 tomato yell
7	222	61.5	349	1 VAL1_PTMV	P38609 tomato yell
8	222	61.5	349	1 VAL1_TYIC	Q06923 pepper bus
9	217	60.1	353	1 VAL1_PTMV	P27260 tomato yell
10	213	59.0	353	1 VAL1_PTMV	P05175 bean golden
11	213	59.0	353	1 VAL1_PTMV	P05175 bean golden
12	210	58.2	361	1 VAL1_TYIC	P04991 tomato yell
13	200	55.4	357	1 VAL1_TYIC	Q06557 tomato yell
14	128	35.5	347	1 VAL1_SLCV	P29048 squash leaf
15	61.5	17.0	299	1 Y175_HELPJ	Q29497 helicobacte
16	61.5	17.0	334	1 G3P_BACST	P00362 bacillus at
17	61.5	17.0	334	1 G3P_BACST	P00362 bacillus at
18	61.5	17.0	1044	1 BURL_SCHPO	Q04753 bacillus co
19	59	16.3	1483	1 CYPL_YEAST	P21351 saccharomyc
20	58.5	16.2	297	1 RRP_PRAVP	P06747 rabies viru
21	58	16.1	492	1 MOT3_MOUSE	Q35308 mus musculu
22	58	16.1	492	1 MOT3_MOUSE	Q35308 mus musculu
23	58	16.1	555	1 GLPD_BACSU	P18158 bacillus su
24	58	16.1	501	1 CY53_BUCAL	P57503 buchneria ap
25	57	15.8	316	1 SPOE_COPFR	Q08447 lactobacill
26	57	15.8	316	1 SPOE_COPFR	Q08447 lactobacill
27	57	15.8	379	1 CYB_ASTPE	Q3318 asterina pe
28	57	15.8	387	1 Y4PF_RHNS	P55615 rhizobium s
29	57	15.8	836	1 GCSR_HUMAN	Q09062 homo sapien
30	57	15.8	1287	1 SK12_YEAST	P35207 saccharomyc
31	56.5	15.7	863	1 AMPN_CAUCR	P37893 caulobacter
32	56	15.5	377	1 LHM4_MOUSE	P53776 mus musculu
33	56	15.5	377	1 LHM4_MOUSE	P53776 mus musculu
					P24400 lactobacill

ALIGNMENTS

RESULT	I	VAL1_TGMV	STANDARD	PRT	352 AA
AC	P03567				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-JUN-1994 (Rel. 29, Last annotation update)				
DE	ALL PROTEIN.				
DE	ACL.				
GN	tomato golden mosaic virus (TGMV).				
OS	Virus; Viridales; Geminiviridae; Begomovirus.				
CC	NCBI_TaxID=10831;				
CC	11				
CC	SEQUENCE FROM N.A.				
CC	Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;				
CC	*Complete nucleotide sequence of the infectious cloned DNA components				
CC	of tomato golden mosaic virus: potential coding regions and regulatory				
CC	sequences. J197-2205(1984).				
CC	----- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY -----				
CC	----- THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	utilized without the permission of the source. See http://www.isb-sib.ch/aboutus/				
CC	or send an email to license@isb-sib.ch				
CC	EMBL; K02029; -: NOT_ANNOTATED_CDS.				
DR	PIR: A04170; Q0CV11.				
DR	InterPro: IPR001191; Gemin1_AL1.				
DR	InterPro: IPR001191; Gemin1_AL1.				
DR	PRINTS: PR00227; GEMCOATCWL1.				
DR	PRINTS: PR00228; GEMCOATCWL1.				
DR	ProDom: PD00736; Gemin1_AL1.				
DR	ATP-binding.				
KW	NP-BIND 223				
FT	ATP (POTENTIAL).				
FT	NP-BIND 352 AA; 40332 MW; C33C938F9644B4A4 CRC64;				
SC	SEQUENCE				
Query Match	95.8%; Score 346; DB 1; Length 352;				
Best Local Similarity	95.7%; Pred. No. 1.1e-33;				
Matches	67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
QY	1 TLVWGEFQVDSARGCCTSDNAAAEALNSKEALQITAAIPKYLFOFHNLNSL 60				
DB	111 TLVWGEFQVDSARGCCTSDNAAAEALNSKEALQITAAIPKYLFOFHNLNSL 170				
QY	61 DRIFDKTPEP 70				
DB	171 DRIFDKTPEP 180				
RESULT	2				
VAL1_PTMV					

```

ID VALL_PYMV STANDARD: PRT: 361 AA.
AC P27258;
DT 01-AUG-1992 (Rel. 23, Created)
DE 01-AUG-1992 (Rel. 23, Last sequence update)
OS ALI PROTEIN (Rel. 23, Last annotation update)
DR P14982;
DE Potato yellow mosaic virus (isolate Venezuela).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10828;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RT Stanley J.F., Roberts E.J.F., Hamilton W.D.O.:
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RT J. Gen. Virol. 72:1515-1520(1991).
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CC -----
CC EMBL: D005940; BAA0782.1;
CC PIR: J00364; Q0CVPT. Geminiviridae;
CC PIR: J00364; Q0CVPT. Geminiviridae;
CC PIR: J00364; Q0CVPT. Geminiviridae;
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00228; GEMCOATCLVL1.
CC ProDom: PD000736; Geminiviridae;
CC ATP-binding. 222 225 ATP (POTENTIAL).
CC NP_BIND
CC SEQUENCE 361 AA; 40650 MW; 5627A35BF1264383 CRC64;
CC
CC Query Match 69.0%; Score 249; DB 1; Length 361;
CC Best Local Similarity 68.1%; Pred. No. 3.6e-22;
CC Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
CC
CC QY 1 TLWGEQVQDSRGAGCGQTSNDAAEALNASSKEPALQITAAATPKYLYFQPHNLSNL 60
DB 110 TIENGLQIDNSAGCGQTSNDAAEALNASSKEPALQITAAATPKYLYFQPHNLSNL 169
OY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178
CC
CC Query Match 69.0%; Score 249; DB 1; Length 361;
CC Best Local Similarity 68.1%; Pred. No. 3.6e-22;
CC Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
CC
CC QY 1 TLWGEQVQDSRGAGCGQTSNDAAEALNASSKEPALQITAAATPKYLYFQPHNLSNL 60
DB 110 TIENGLQIDNSAGCGQTSNDAAEALNASSKEPALQITAAATPKYLYFQPHNLSNL 169
OY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178
CC
CC RESULT 3
CC VALL_CLVKN STANDARD: PRT: 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DE 01-APR-1990 (Rel. 14, Last sequence update)
OS ALI PROTEIN (Rel. 29, Last annotation update)
DR P14982;
DE Cassava latent virus (strain West Kenyan 844).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10818;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174330; PubMed=2306831;
RT Stanley J.F., Roberts E.J.F., Hamilton W.D.O.:
RT "The nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RT Nucleic Acids Res. 18:197-198(1990).
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CC -----
CC EMBL: X17095; CAA34953.1;
CC PIR: 07594; Q0CVPT. Geminiviridae;
CC PIR: 07594; Q0CVPT. Geminiviridae;
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00228; GEMCOATCLVL1.
CC ProDom: PD000736; Geminiviridae;
CC ATP-binding. 220 227 ATP (POTENTIAL).
CC NP_BIND
CC SEQUENCE 358 AA; 40435 MW; 1D16B0C82A5E2C CRC64;
CC
CC Query Match 66.5%; Score 240; DB 1; Length 358;
CC Best Local Similarity 61.4%; Pred. No. 4.2e-21;
CC Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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CC -----
CC EMBL: J02057; -- NOT ANNOTATED CDS.
CC PIR: J02057; Q0CVPT. Geminiviridae;
CC PIR: J02057; Q0CVPT. Geminiviridae;
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00228; GEMCOATCLVL1.
CC ProDom: PD000736; Geminiviridae;
CC ATP-binding. 220 227 ATP (POTENTIAL).
CC NP_BIND
CC SEQUENCE 358 AA; 40346 MW; ED17E755E92D69 CRC64;
CC
CC Query Match 66.5%; Score 240; DB 1; Length 358;
CC Best Local Similarity 61.4%; Pred. No. 4.2e-21;
CC Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
CC
CC QY 1 TLWGEQVQDSRGAGCGQTSNDAAEALNASSKEPALQITAAATPKYLYFQPHNLSNL 60
DB 109 TVENGQQLIDNSAGCGQTSNDAAEALNASSKEPALQITAAATPKYLYFQPHNLSNL 168
OY 61 DRIFDKTPE 70
DB 169 DRIFDKPEPP 178
CC
CC RESULT 4
CC VALL_CLVKN STANDARD: PRT: 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DE 01-APR-1990 (Rel. 14, Last sequence update)
OS ALI PROTEIN (Rel. 29, Last annotation update)
DR P14972;
DE Cassava latent virus (strain Nigerian).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10819;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174330; PubMed=2306831;
RT Stanley J.F., Roberts E.J.F., Hamilton W.D.O.:
RT "The nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain).";
RT Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC -----
CC EMBL: X17095; CAA34953.1;
CC PIR: 07594; Q0CVPT. Geminiviridae;
CC PIR: 07594; Q0CVPT. Geminiviridae;
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00227; GEMCOATALL1.
CC PRINTS: PR00228; GEMCOATCLVL1.
CC ProDom: PD000736; Geminiviridae;
CC ATP-binding. 220 227 ATP (POTENTIAL).
CC NP_BIND
CC SEQUENCE 358 AA; 40435 MW; 1D16B0C82A5E2C CRC64;
CC
CC Query Match 66.5%; Score 240; DB 1; Length 358;
CC Best Local Similarity 61.4%; Pred. No. 4.2e-21;
CC Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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QY 1 TLWGEFQVDSARGSCOTSNDAAAEALNASKEALQIIAAIAPEKYLQFHNLSNL 60
DB 109 TLWGEFQVDSARGSCOTSNDAAAEALNASKEALQIIAAIAPEKYLQFHNLSNL 168
QY 61 DRIFDKTPEP 70
DB 169 DRIFQEPFAP 178

RESULT 5
VALL TYLCA
ID VALL TYLCA STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DB 109 TYLCA (C1 PROTEIN).
DB 169 TYLCA (C1 PROTEIN).
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxId=36447;
RX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=9513978; PubMed=6423446;
RX J. Gen. Virol. 74:147-151(1993).
RT "Nucleotide sequence and genome organization of Tomato leaf curl
    geminivirus."
RL -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
RC PIR: J01887; J01887.
DR InterPro: IP0001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRODOM; PD000736; Gemini_AL1; 1.
DR ATP-binding.
KW ATP-binding.
KW NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 34367184B704098 CRC64;

Query Match 64.5%; Score 233; DB 1; Length 362;
Best Local Similarity 54.18; Pred. No. 2,9620;
Matches 46; Conservative 9; Mismatches 14; Indels 15; Gaps 1;

QY 1 TLWGEFQVDSARGSCOTSNDAAAEALNASKEALQIIAAIAPEKYLQFHNLSNL 60
DB 110 TLWGEFQVDSARGSCOTSNDAAAEALNASKEALQIIAAIAPEKYLQFHNLSNL 169
QY 61 DRI-----FKTPEP 69
DB 170 DRIPTPLVVVSPFISSFDVPE 194

RESULT 6
VALL TYLCA
ID VALL TYLCA STANDARD; PRT; 359 AA.
AC P3560;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
DB 109 TYLCA (C1 PROTEIN).
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxId=37139;
RX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=94256836; PubMed=8198442;
RX Norris E., Hidalgo E., Accotto G., Moriones E.;
    "High similarity among the tomato yellow leaf curl virus isolates
    from the west Mediterranean basin: the nucleotide sequence of an
    infectious clone from Spain."

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RL Arch. Virol. 135:165-170(1994).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC EMBL: Z5751; CAB51026.1;
CC PIR: S39211; S39211.
CC InterPro: IP0001191; Gemini_AL1.
CC Pfam: PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC PRODOM; PD000736; Gemini_AL1; 1.
CC ATP-binding.
CC NP_BIND 221 228 ATP (POTENTIAL).
CC SEQUENCE 359 AA; 41065 MW; 2D170A51E8B0A38C CRC64;

Query Match 63.4%; Score 229; DB 1; Length 359;
Best Local Similarity 60.94; Pred. No. 8,6e-20;
Matches 42; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWNGEFQVDSARGSCOTSNDAAAEALNASKEALQIIAAIAPEKYLQFHNLSNL 61
DB 111 LEWGTGFDGSRGGQOTANDAYAKAINAGSKSEALDVIKELAPDYILHFNLSNL 170
QY 62 RIFDKTPEP 70
DB 171 RVFQVFPAP 179

RESULT 7
VALL PHUV
ID VALL PHUV STANDARD; PRT; 349 AA.
AC O06923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
GN AL1.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
ON NCBI_TaxId=28349;
RX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=94015007; PubMed=8409944;
RX Torres-Pacheco I., Carzon-Tiznado J.A., Herrera-Estrella L.,
    Rivera-Bustamante R.P.;
    "Complete nucleotide sequence of pepper huasteco virus: analysis and
    comparison with bipartite geminiviruses."
RT J. Gen. Virol. 74:2225-2231(1993).
RL -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC EMBL: Y70418; G344956.1;
CC PIR: S31875; S31875.
CC InterPro: IP0001191; Gemini_AL1.
CC Pfam: PF00799; Gemini_AL1; 1.
CC PRINTS; PR00227; GEMCOATL1.
CC PRODOM; PD00228; GEMCOATL1.

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DR ProDom: PD000736; Gemini_AL1; 1.
KW NP_BIND 221 228 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 39722 MW; 52F4E76CD56370F4 CRC64;

Query Match
Best Local Similarity 61.5%; Score 222; DB 1; Length 349;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLVWGFQVDSRGSGCOTSDAAAEALNASSKEPALQITAAAIPEKYLQFPHNLSNL 60
DB 110 TWMEQFQIDGRSGQGSANDTYAKALNASSAEAEQITKEEQPHQFFLQPHNIVSNA 169

OY 61 DRIFKTPPEP 70
DB 170 NRIFQTPPEP 179

RESULT 8
VAL1_TLVCW
AC P22760; STANDARD; PRT: 359 AA.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
GN Clinto yellow leaf curl virus (strain Maryland) (YLCV).
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10833;
RA [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-9210760; PubMed=18400676;
RX Kheyri-Four A., Bendahmane M., Matzelt V., Accotto G.P., Crespi S.,
RA "Tomato yellow leaf curl virus from Sardinia is a
RT whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC EMBL: M10070; AAA46318.1;
CC InterPro: IPR001191; Gemini_AL1.
CC Pfam: PF00799; Gemini_AL1; 1.
CC PRINTS: PR00227; GEMCOATL1.
CC PROSITE: PS00228; GEMCOATL1.
CC ProDom: PD000736; Gemini_AL1; 1.
KW ATP-binding, 220 227 ATP (POTENTIAL).
SQ SEQUENCE 355 AA; 40733 MW; 9716A07C59FEA7 CRC64;

Query Match
Best Local Similarity 58.0%; Score 222; DB 1; Length 359;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

OY 2 LKRGFQVDSRGSGCOTSDAAAEALNASSKEPALQITAAAIPEKYLQFPHNLSNL 61
DB 111 LKMGTFQIDGRSGQGSANDTYAKALNASSGSAOLDVKELPADPYLVHFNHNSLD 170

OY 62 DRIFKTPPEP 70
DB 171 KVFQVPPAP 179

Query Match
Best Local Similarity 61.5%; Score 222; DB 1; Length 359;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

OY 1 TLVWGFQVDSRGSGCOTSDAAAEALNASSKEPALQITAAAIPEKYLQFPHNLSNL 60
DB 110 TWMEQFQIDGRSGQGSANDTYAKALNASSAEAEQITKEEQPHQFFLQPHNIVSNA 169

OY 61 DRIFKTPPEP 70
DB 170 NRIFQTPPEP 179

RESULT 10
VAL1_ABMWV
AC P21947; STANDARD; PRT: 355 AA.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 01-JUN-1991 (Rel. 22, Last annotation update)
DE AL1 PROTEIN.
GN AC1.
OS Abutilon mosaic virus (Isolate West India).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10816;
RA [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-91020984; Pubmed-2219703;
RX Frischmuth T., Zimmat G., Jeske H.;
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
as well as eukaryotic features.";
RT Virology 178:461-468(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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CC -----
DR EMBL: X15983; -. NOT_ANNOTATED_CDS.
DR EMBL: X62144; GenBank.
DR InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD00228; GEMCOATCLV1.
DR ATP-Binding. 221 228 ATP (POTENTIAL).
KT NP-BIND. 222 229
SQ SEQUENCE 355 AA; 40257 MW; 16A2CABA66231E95 CRC64;

Query Match 59.8%; Score 216; DB 1; Length 355;
Best Local Similarity 58.6%; Pred. NO. 3e-18;
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 1 TLVWGFQVGRSGCGCTSDNAAEAALNASKEALQITAAATPEKYLQFHNLNSL 60
Db 110 TIWGEFQVGRSGCGCTSDNAAEAALNASKEALQITAAATPEKYLQFHNLNSL 169
Qy 61 DRIFDKTPPE 70
Db 170 ERIFAKAPEP 179

RESULT 11
ID VALL_BCTV STANDARD; PRT; 358 AA.
AC P14931;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE ALL PROTEIN (40.8 KDA PROTEIN).
CC Vest. curly top virus (ACTV).
CC Vest. curly top viruses; Geminiviridae; Curtovirus.
CC NCBI_TaxID=10840;
RN [1]
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
EMBO J. 5:1561-1570 (1986).
CC -----
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CC -----
DR EMBL: X04144; -. NOT_ANNOTATED_CDS.
DR InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD00730; Gemini.AL1.1.
DR ATP-Binding. 222 229
KT NP-BIND. 222 229 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 40889 MW; 39A45F3C0B9C333 CRC64;

Query Match 59.0%; Score 213; DB 1; Length 358;

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Best Local Similarity 55.7%; Pred. NO. 6.8e-18;
Matches 39; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGFQVGRSGCGCTSDNAAEAALNASKEALQITAAATPEKYLQFHNLNSL 60
Db 110 TIWGEFQVGRSGCGCTSDNAAEAALNASKEALQITAAATPEKYLQFHNLNSL 169
Qy 61 DRIFDKTPPE 70
Db 170 ERIFAKAPEP 179

RESULT 12
ID VALL_TMOV STANDARD; PRT; 361 AA.
AC Q06657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALL PROTEIN.
CC ALL.
CC Tomato mottle virus (Isolate Florida) (TMOV).
CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
CC NCBI_TaxID=36449;
RN [1]
RA MCELINGE 93107858; Pubmed=14659361.
RX KX
CC "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229 (1992).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: L14460; AAC32414.1; -.
DR EMBL: X01679; GenBank.
DR InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD00228; GEMCOATCLV1.
DR ATP-Binding. 222 229
KT NP-BIND. 222 229 ATP (BY SIMILARITY).
SQ SEQUENCE 361 AA; 40516 MW; 813BB65CEAC6950 CRC64;

Query Match 58.2%; Score 210; DB 1; Length 361;
Best Local Similarity 54.3%; Pred. NO. 1.6e-17;
Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TLVWGFQVGRSGCGCTSDNAAEAALNASKEALQITAAATPEKYLQFHNLNSL 60
Db 110 TIWGEFQVGRSGCGCTSDNAAEAALNASKEALQITAAATPEKYLQFHNLNSL 169
Qy 61 DRIFDKTPPE 70
Db 170 ERIFAKAPEP 179

RESULT 13
ID VALL_TYLCV STANDARD; PRT; 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE GN ALL PROTEIN (C1 PROTEIN).
OC Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RR SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeldan M., Zamir D., Czosnek H.;
RT *Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.*;
RL Virology 185:151-161(1991).
RL --- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC ---
CC EMBL; X15656; CAA33688.1;
DR PIR: D40779; QOCVCL.
DR InterPro: IPR001191; Gemin_LALI.
DR PRINTS: PF00799; Gemin_LALI.1.
DR PROSITE: PS00227; GEMCATALI.1.
DR PRODOM: PD000736; Gemin_LALI.1.
KW ATP-binding.
KW NP_BIND.
KW FT SEQUENCE 357 AA; 40678 MW; 939A68E1AB3E2A7 CRC64;
SQ
Query Match 55.4%; Score 200; DB 1; Length 357;
Best Local Similarity 33.4%; Pred. No. 8.2e-08;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
CC
OY 4 WEEQVDRSARGCGCSTNDAAEALNASSKEALQITAAAIPEKYLFOFHNLSNLDRI 63
DB 111 FGVQSDIGRSARGCGSANDAYAEALNSGSKSEALNLIKKEAPKDYILOFHNLSNLDRI 170
OY 64 F 64
DB 171 F 171
RESULT 14
VALL_SLCV STANDARD; PRT; 347 AA.
ID VALL_SLCV
CD 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALL PROTEIN.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10823;
RR SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdins I.B.;
RT *Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.*;
RL Virology 160:58-69(1991).
RL --- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC ---
CC EMBL; M38183; AAC32410.1; ALT_INIT.
DR PIR: C36785; QOCVSL.
DR InterPro: IPR001191; Gemin_LALI.
DR PRINTS: PF00799; GEMCATALI.1.
DR PROSITE: PS00227; GEMCATALI.1.
DR PRODOM: PD000736; Gemin_LALI.1.
KW ATP-binding.
KW NP_BIND.
KW FT SEQUENCE 347 AA; 39110 MW; ADEAD9DEE122110E CRC64;
SQ
Query Match 35.5%; Score 128; DB 1; Length 347;
Best Local Similarity 39.4%; Pred. No. 8.2e-08;
Matches 26; Conservative 13; Mismatches 23; Indels 4; Gaps 1;
CC
OY 5 GFEQVDRSARGCGCSTNDAAEALNASSKEALQITAAAIPEKYLFOFHNLSNLDRI 64
DB 111 FGVQSDIGRSARGCGSANDAYAEALNSGSKSEALNLIKKEAPKDYILOFHNLSNLDRI 171
OY 65 DKTPEP 70
DB 172 OKPPEP 177
RESULT 15
Y175_HELPJ STANDARD; PRT; 299 AA.
ID Y175_HELPJ
CD 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN JHP0161 PRECURSOR.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RR SEQUENCE FROM N.A.
RX MEDLINE=9923682;
RA Alim R., Isiguz L.S., Moir D.T., King B.L., Brown E.D., Deig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT *Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.*;
RL Nucleic Acids Res. 29:101-109(2001).
RL --- SIMILARITY: BELONGS TO THE PPTC/PARVULIN FAMILY OF ROTAMASES.
CC STRONG. TO C.JEJUNI CBP2.
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CC ---
CC EMBL; AE001454; AAD05744.1;
DR HSSP: Q13526; IPIN.
DR InterPro: IPR000297; Rotamase.
DR PRINTS: PS01036; PPTC_PP1ASEL.1.
DR PROSITE: PS00639; Rotamase; 1.
KW HYPOTHETICAL PROTEIN JHP0161 PRECURSOR.
KW SIGNAL 22 299 HYPOTHETICAL PROTEIN JHP0161.
FT CHAIN 22 299
FT DOMAIN 154 253 PPTC-LIKE.
SQ SEQUENCE 299 AA; 34040 MW; 9C037B1CD110143 CRC64;

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DE GN ALL PROTEIN (C1 PROTEIN).
OC Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RR SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeldan M., Zamir D., Czosnek H.;
RT *Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.*;
RL Virology 185:151-161(1991).
RL --- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC ---
CC EMBL; X15656; CAA33688.1;
DR PIR: D40779; QOCVCL.
DR InterPro: IPR001191; Gemin_LALI.
DR PRINTS: PF00799; Gemin_LALI.1.
DR PROSITE: PS00227; GEMCATALI.1.
DR PRODOM: PD000736; Gemin_LALI.1.
KW ATP-binding.
KW NP_BIND.
KW FT SEQUENCE 357 AA; 40678 MW; 939A68E1AB3E2A7 CRC64;
SQ
Query Match 55.4%; Score 200; DB 1; Length 357;
Best Local Similarity 33.4%; Pred. No. 8.2e-08;
Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
CC
OY 4 WEEQVDRSARGCGCSTNDAAEALNASSKEALQITAAAIPEKYLFOFHNLSNLDRI 63
DB 111 FGVQSDIGRSARGCGSANDAYAEALNSGSKSEALNLIKKEAPKDYILOFHNLSNLDRI 170
OY 64 F 64
DB 171 F 171
RESULT 14
VALL_SLCV STANDARD; PRT; 347 AA.
ID VALL_SLCV
CD 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALL PROTEIN.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10823;
RR SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RA Lazarowitz S.G., Lazdins I.B.;
RT *Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.*;
RL Virology 160:58-69(1991).
RL --- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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Query Watch      17.04; Score 61.5; DB 1; Length 299;
Best Local Similarity 28.1%; Pred. No. 5.5;
Matches 19; Conservative 12; Mismatches 13; Indels 21; Gaps 2;

QY 22 NDAAAALNLS-----SREBA-LOITAAAPKYLQFQINLSNLR 62
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 93 NDAKAKLNTPEFKAMNKKQALVEFKARQNEVKKIQLPEKQDPI--NANKQ 150
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QY 63 IFDK 66
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Db 151 LFVK 154

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Search completed: January 3, 2002, 15:57:15
Job time: 1101 sec

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2	281	77.8	226	12	Q09727	tomato rug
3	281	77.8	226	12	Q9WHF5	tomato mild
4	279	77.3	361	12	Q67574	bean golden
5	277	76.7	225	12	Q9QDB1	cowpea gold
6	274	75.9	314	12	Q9E1F8	sweet potato
7	274	75.9	364	12	Q9Q555	sweet potato
8	271	75.1	185	12	Q9H653	sweet potato
9	266	73.7	149	12	Q9E1A5	sida golden
10	266	73.7	233	12	Q9RT44	macrotillu
11	260	72.0	234	12	Q93180	potato yell
12	234	70.4	190	12	Q92089	tobacco lea
13	234	70.4	190	12	Q92084	tobacco lea
14	233	70.1	208	12	Q97024	tobacco lea
15	263	70.1	208	12	Q97024	tobacco lea
16	251	69.5	208	12	Q920C0	tobacco lea
17	251	69.5	208	12	Q920C0	tobacco lea
18	251	69.5	363	12	Q72705	cotton leaf
19	251	69.5	363	12	Q72719	cotton leaf

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Db 111 TIEWGFQIDGRSGAQGTANDAAAEALNASSKEAARIKEKLPKLPFYHNLSSNLI 172
Qy 61 DTRFDKTPPE 70
Db 171 DRIFAKAPEP 180

RESULT 4
ID AC 067574 PRELIMINARY: PRT: 361 AA.
AC 067574:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE POTANTIE REPLICATIVE PROTEIN.
DE
DE
Qs Bean golden mosaic virus
Qs
Qc Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
Ox NCBI_TaxID=10839;
[1]
RN
SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RA J2. Virology 81:980-985(1991).
RM
SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RA Plant Dis. 75:336-342(1991).
RL
[3]
RN
SEQUENCE FROM N.A. Faria J.C., Ahlquist P.G., Maxwell D.P.;
RN Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M88686; AAA66312.1; -
DR InterPro: IPR001191; Gemini_A11.
DR Pfam: PF00789; Gemini_A11.1.
DR PRINTS: PD00227; GEMCOATALL.
DR Prodom: PD000736; Gemini_A11.1.
DR SEQUENCE 361 AA; 41041 MW; 0.094C7ACAF068788 CRC64;
Sg

Query Match 77.3%; Score 279; DB 12; Length 361;
Best Local Similarity 77.5%; Pred. No. 9e-25;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps

Qy 4 WGEFQVGRSGAQGTSDNAAAEALNASSKEAALQIAAIIPKYLQFPHNLSSNLDRI 63
113 WGEFQVGRSGAQGTANDAAAEALNASSKEAARIKEKLPKLPFYHNLSSNLDRI 172
Qy 64 FDKTPEP 70
Db 173 FTKAPEP 179

RESULT 5
ID Q9QDB1 PRELIMINARY: PRT: 225 AA.
AC Q9QDB1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (RACANT).
DE
DE
Qs Cowpea golden mosaic geminivirus.
Qs
Qc Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
Ox NCBI_TaxID=6926;
[1]
RN
SEQUENCE FROM N.A.
RA STRAIN=CGW4-BR;
RA Faria J.C.;
RA Brazili.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN

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10

10

2004

ID PB8975 PRELIMINARY: PRT: 149 AA.
 AC 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN A1.
 OS Macrotidium golden mosaic geminivirus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=51676;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.;
 RL Thesis (1996). Biochemistry, University of the West Indies, Jamaica.
 RL EMBL: U75278; AAR36919.1;
 DR InterPro: IPRO01191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; GeminI_AL1; 1.
 DR NON_TER 149 149
 FT SEQUENCE 149 AA: 16785 MW; E4CF5ED4C9CD508 CRC64;
 SQ SEQUENCE 149 AA: 16785 MW; E4CF5ED4C9CD508 CRC64;

Query Match
 Best Local Similarity 73.7%; Score 266; DB 12; Length 149;
 Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 TLVGEFQVDSRGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 60
 Db 52 TTEGTFQIDGRSARGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 111
 Oy 61 DRIFDKTPPEP 70
 Db 112 DRIFDKTPPEP 121
 RESULT 10
 ID OSYL44 PRELIMINARY: PRT: 233 AA.
 AC 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Macrotidium golden mosaic geminivirus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=51676;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.;
 RL "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.;
 RL "Molecular characterization of two distinct geminiviruses infecting M. lachryoides from Jamaica."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A009780.1; GeminI_AL1.
 DR InterPro: IPRO01191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; GeminI_AL1; 1.
 DR NON_TER 233 233
 FT SEQUENCE 233 AA: 26355 MW; AM490AF4D2166A02 CRC64;
 SQ SEQUENCE 233 AA: 26355 MW; AM490AF4D2166A02 CRC64;

Query Match
 Best Local Similarity 70.0%; Score 260; DB 12; Length 234;
 Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
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 Db 110 TTEGTFQIDGRSARGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 169
 Oy 61 DRIFDKTPPEP 70
 Db 170 DRIFDKTPPEP 179
 RESULT 12
 ID OS2089 PRELIMINARY: PRT: 190 AA.
 AC Q92089
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE C-TERMINAL REGION OF THE GEMINIVIRUS GEMINIVIRUS (FRAGMENT).
 GN C1.
 OS tobacco leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=67762;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-YOKOHAMA3;
 RA OOL K.;
 RL "Molecular phylogeny of geminivirus infecting wild plants in Japan."
 RL J. Plant Res. 110:247-257(1997).
 DR EMBL: AB001315; BAA34033.1;
 DR InterPro: IPRO01191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1; 1.

Query Match
 Best Local Similarity 73.7%; Score 266; DB 12; Length 233;
 Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 TLVGEFQVDSRGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 60
 Db 110 TTEGTFQIDGRSARGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 169
 Oy 61 DRIFDKTPPEP 70
 Db 170 DRIFDKTPPEP 179
 RESULT 11
 ID OS3180 PRELIMINARY: PRT: 234 AA.
 AC Q39180
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=10827;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-TONATO STRAIN;
 RA Guzman P.; Arredondo C.R.; Emmatty D.; Portillo R.J.; Gilbertson R.L.;
 RL EMBL: AF024553; AAB42405.1;
 DR InterPro: IPRO01191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; GeminI_AL1; 1.
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 SQ SEQUENCE 234 AA: 26486 MW; 9DBDF0697105CD19 CRC64;

Query Match
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 Db 110 TTEGTFQIDGRSARGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 169
 Oy 61 DRIFDKTPPEP 70
 Db 170 DRIFDKTPPEP 179
 RESULT 12
 ID OS2089 PRELIMINARY: PRT: 190 AA.
 AC Q92089
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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 GN C1.
 OS tobacco leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=67762;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-YOKOHAMA3;
 RA OOL K.;
 RL "Molecular phylogeny of geminivirus infecting wild plants in Japan."
 RL J. Plant Res. 110:247-257(1997).
 DR EMBL: AB001315; BAA34033.1;
 DR InterPro: IPRO01191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1; 1.

Query Match
 Best Local Similarity 70.0%; Score 266; DB 12; Length 149;
 Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
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 Db 52 TTEGTFQIDGRSARGSGCOTSDNAAEALNASSKEALQIIAAATPKYLFQFHNLSNL 111
 Oy 61 DRIFDKTPPEP 70
 Db 112 DRIFDKTPPEP 121
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 ID OSYL44 PRELIMINARY: PRT: 233 AA.
 AC 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Macrotidium golden mosaic geminivirus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 ON NCBI_TaxID=51676;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.;
 RL "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.;
 RL "Molecular characterization of two distinct geminiviruses infecting M. lachryoides from Jamaica."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A009780.1; GeminI_AL1.
 DR InterPro: IPRO01191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1; 1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR ProDom: PD000736; GeminI_AL1; 1.
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 FT SEQUENCE 233 AA: 26355 MW; AM490AF4D2166A02 CRC64;
 SQ SEQUENCE 233 AA: 26355 MW; AM490AF4D2166A02 CRC64;

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DR PRINTS: PR00227; GEMCOATALL.
DR Prodom: PD000736; Gemini_All; 1.
DR NON_TER 190 190
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SQ SEQUENCE 190 AA: 21432 MW: AAC093D1D1610FAD CRC64:

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Best Local Similarity 58.4%; Pred. No. 3.8e-22;
Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

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DB 1 TLVWGEFQVDSRGSGCOTSDAAAEALNASSKEALQIIAAAIPEKYLQFQHNLSNL 60
DB 85 TLEWGTFOVDSRGSGCCONDAACAALNASSKAALAIIREKLPKDFIFOYHNLSNL 144
OY 61 DRI-----FQKTPPE 69
DB 145 DRIAPLEVFVCPPTASSSFDOVPE 169

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AC Q92084; 1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
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DR PRINTS: PR000736; Gemini_All; 1.
DR Prodom: PD000736; Gemini_All; 1.
FT NON_TER 190 190
SQ SEQUENCE 190 AA: 21444 MW: AAC1C2943E3F01AD CRC64:

Query Match 70.4%; DB 12; Length 190;
Best Local Similarity 58.4%; Pred. No. 3.8e-22;
Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

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DB 85 TLEWGTFOVDSRGSGCCONDAACAALNASSKAALAIIREKLPKDFIFOYHNLSNL 144
OY 61 DRI-----FQKTPPE 69
DB 145 DRIAPLEVFVCPPTASSSFDOVPE 169

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AC Q94827; 1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
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DR PRINTS: PR000736; Gemini_All; 1.
DR Prodom: PD000736; Gemini_All; 1.
FT NON_TER 190 190
SQ SEQUENCE 190 AA: 21444 MW: AAC1C2943E3F01AD CRC64:

Query Match 70.4%; DB 12; Length 190;
Best Local Similarity 58.4%; Pred. No. 3.8e-22;
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DB 145 DRIAPLEVFVCPPTASSSFDOVPE 169

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DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
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DR PRINTS: PR000736; Gemini_All; 1.
DR Prodom: PD000736; Gemini_All; 1.
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SQ SEQUENCE 208 AA: 23526 MW: 249CC31D8729C72D CRC64:

Query Match 70.1%; DB 12; Length 208;
Best Local Similarity 58.8%; Pred. No. 5.5e-22;
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OY 61 DRI-----FQKTPPE 69
DB 162 DRIAPLEVFVCPPTASSSFDOVPE 186

Search completed: January 3, 2002, 15:56:25

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Fri Jan 4 09:38:21 2002

us-09-289-346a-4.rspt

Page 6

Job time: 1121 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:49 ; Search time 65.28 Seconds
(without alignments)
24,130 Million cell updates/sec

File: US-09-289-346a-4

Perfect score: 361

Sequence: 1 TLWKEFQVDSRARGSCQT.....POFHNLNLDRIFDKTEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA*:

- 1: /cgn2_5/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_5/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_5/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_5/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_5/ptodata/2/1aa/6C_COMB.pep.*
- 6: /cgn2_5/ptodata/2/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	222	61.5	359	4	US-08-809-1038-2	Sequence 2, Appl
2	222	61.5	359	4	US-08-809-1038-2	Sequence 4, Appl
3	222	61.5	359	4	US-08-809-1038-6	Sequence 6, Appl
4	222	61.5	359	4	US-08-809-1038-6	Sequence 6, Appl
5	219	60.7	353	4	US-08-838-151A-44	Sequence 44, Appl
6	219	60.7	353	4	US-08-838-151A-46	Sequence 46, Appl
7	219	60.7	353	4	US-08-838-151A-49	Sequence 49, Appl
8	219	60.7	353	4	US-08-838-151A-52	Sequence 52, Appl
9	219	60.7	353	4	US-08-838-151A-55	Sequence 55, Appl
10	214	59.3	361	4	US-08-838-151A-2	Sequence 2, Appl
11	214	59.3	361	4	US-08-838-151A-6	Sequence 6, Appl
12	214	59.3	361	4	US-08-838-151A-6	Sequence 6, Appl
13	214	59.3	361	4	US-08-838-151A-8	Sequence 8, Appl
14	200	55.4	357	4	US-08-838-151A-24	Sequence 24, Appl
15	200	55.4	357	4	US-08-838-151A-27	Sequence 27, Appl
16	200	55.4	357	4	US-08-838-151A-30	Sequence 30, Appl
17	192	53.2	357	4	US-08-838-151A-20	Sequence 20, Appl
18	60.5	16.8	131	4	US-08-838-151A-14	Sequence 14, Appl
19	60.5	16.8	134	6	529069011562-1	Patent No. 529069011562-1
20	57	15.8	771	6	US-08-413-052-6	Sequence 6, Appl
21	57	15.8	771	6	US-08-413-052-6	Sequence 6, Appl
22	57	15.8	771	6	US-07-923-976-6	Sequence 6, Appl
23	57	15.8	783	6	5422248-2	Patent No. 5422248-2
24	57	15.8	836	1	US-07-923-976-4	Sequence 4, Appl
25	57	15.8	863	1	US-07-923-976-8	Sequence 8, Appl
26	55	15.2	783	6	5231168-2	Patent No. 5231168-2
27	54.5	15.1	258	4	US-09-251-645-5	Sequence 5, Appl

Sequence 24, Appl
Sequence 24, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 4, Appl
Sequence 13, Appl
Sequence 4, Appl
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Sequence 16, Appl
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Sequence 2, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 2, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-809-1038-2
; Sequence 2, Application US/08809103B
; Patent No. 6135507
; GENE INFORMATION:
; APPLICANT: GROENBORN, Rutno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AS YOUNG & THOMPSON
; STREET: 145 South 23rd Street
; CITY: Virginia
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: SYSTRAN/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: IN 94,11040
; FILING DATE: 1-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/01192
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 2,925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TOPOLOGY: 1
; MOLECULE TYPE: protein
US-08-809-1038-2

Query Match 61.5%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 3.2e-22;

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Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 RIFKQTPPEP 70
    :|||
Db 171 KVFQVPPAP 179

RESULT 2
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; PRIORITY APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIORITY APPLICATION DATA: NO PCT/FR95/01192
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 61.5%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 3.2e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 61
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Db 111 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 RIFKQTPPEP 70
    :|||
Db 171 KVFQVPPAP 179

RESULT 3
US-08-809-103B-4
; Sequence 4, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; PRIORITY APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIORITY APPLICATION DATA: NO PCT/FR95/01192
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 61.5%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 3.2e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 RIFKQTPPEP 70
    :|||
Db 171 KVFQVPPAP 179

RESULT 4
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; PRIORITY APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIORITY APPLICATION DATA: NO PCT/FR95/01192
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 61.5%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 3.2e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 RIFKQTPPEP 70
    :|||
Db 171 KVFQVPPAP 179

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US-08-809-103B-6
; Sequence 6, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; PRIORITY APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIORITY APPLICATION DATA: NO PCT/FR95/01192
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-6

Query Match 61.5%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 3.2e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 RIFKQTPPEP 70
    :|||
Db 171 KVFQVPPAP 179

RESULT 4
US-08-809-103B-8
; Sequence 8, Application US/08809103B
; Patent No. 6133505
; GENERAL INFORMATION:
; APPLICANT: GRONENBORN, Bruno
; TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
; TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; FILING DATE: 17-MAR-1997
; PRIORITY APPLICATION NUMBER: US/08/809,103B
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1994
; PRIORITY APPLICATION DATA: NO PCT/FR95/01192
; APPLICATION NUMBER: FR 94.11040
; FILING DATE: 15-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 685-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 61.5%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 3.2e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 111 LVWGEFQDGRSARGCQTSNDAAEALNASSKEEALQIIAAAIPEKYLFOFHNLNSLD 170
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 62 RIFKQTPPEP 70
    :|||
Db 171 KVFQVPPAP 179

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: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/409,103B
: FILING DATE: 17 MAR 1997
: COUNTRY: U.S.A.
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94,11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J.
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: US94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: (703) 685-0573
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 359 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-809-103B-8

Query Match 61.58; Score 222; DB 4; Length 359;
Best Local Similarity 58.08; Pred. No. 3,2e-22;
Matches 40; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LVWGFEQVDRSGRCGQCTSDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSLD 61
Db 111 LVWGFEQVDRSGRCGQCTSDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSLD 170

Oy 62 DRIFQKTPPEP 70
Db 171 KVFQVPPAP 179

RESULT 5
US-08-838-151A-44
Sequence 44; Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Alquist, Paul
APPLICANT: Alquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5400
: INFORMATION FOR SEQ ID NO: 44:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 353 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-838-151A-44

Query Match 60.74; Score 219; DB 4; Length 353;
Best Local Similarity 60.08; Pred. No. 8.1e-22;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Oy 1 TLVWGFEQVDRSGRCGQCTSDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSNL 60
Db 110 TLVWGFEQVDRSGRCGQCTSDAAAEALNASSKEEALQITAAAIPEKYLQFPHNLSNL 169

Oy 61 DRIFQKTPPEP 70
Db 170 ERIFQKVPPEP 179

RESULT 6
US-08-838-151A-46
Sequence 46; Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Alquist, Paul
APPLICANT: Alquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-45

Query Match 60.7%; Score 219; DB 4; Length 353;
Best Local Similarity 60.0%; Pred. No. 8.le-22;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLVNGEFQVDRSGCGCOTSNDAAEALNASSKEALQITAAATPKYLFQFHNSNL 60
DB 110 TLVNGEFQVDRSGCGCOTSNDAAEALNASSKEALQITAAATPKYLFQFHNSNL 60
OY 61 DRIFDKTPPEP 70
DB 170 ERIFVKVPEP 179

RESULT 7
US-08-838-151A-49
Sequence 55; Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milomow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 60.7%; Score 219; DB 4; Length 353;
Best Local Similarity 60.0%; Pred. No. 8.le-22;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLVNGEFQVDRSGCGCOTSNDAAEALNASSKEALQITAAATPKYLFQFHNSNL 60
DB 110 TLVNGEFQVDRSGCGCOTSNDAAEALNASSKEALQITAAATPKYLFQFHNSNL 60
OY 61 DRIFDKTPPEP 70
DB 170 ERIFVKVPEP 179

DB 170 ERIFVKVPEP 179

RESULT 8
US-08-838-151A-52
Sequence 55; Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milomow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TOPOLGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

Query Match 60.7%; Score 219; DB 4; Length 353;
Best Local Similarity 60.0%; Pred. No. 8.le-22;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLVNGEFQVDRSGCGCOTSNDAAEALNASSKEALQITAAATPKYLFQFHNSNL 60
DB 110 TLVNGEFQVDRSGCGCOTSNDAAEALNASSKEALQITAAATPKYLFQFHNSNL 169
OY 61 DRIFDKTPPEP 70
DB 170 ERIFVKVPEP 179

RESULT 9
US-08-838-151A-55
Sequence 55; Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes

```

;
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

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Query Match 60.74; Score 219; DB 4; Length 353;
Best Local Similarity 60.06; Pctid: No. 8.1e-22;
Matches 42; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

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QY 1 TLVWGFEQVDCRSARGGCGTSDNDAAEALNASSKEEAQIITAAATPEKYLQFPHNLSNL 60
DB 110 TLWGFEQVDCRSARGGCGTSDNDAAEALNASSKEEAQIITAAATPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 170 ERIFDKTPEP 179

```

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RESULT 10
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stoult, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

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; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

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Query Match 59.38; Score 214; DB 4; Length 361;
Best Local Similarity 55.74; Pctid: No. 4e-21;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

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QY 1 TLVWGFEQVDCRSARGGCGTSDNDAAEALNASSKEEAQIITAAATPEKYLQFPHNLSNL 60
DB 110 TLWGFEQVDCRSARGGCGTSDNDAAEALNASSKEEAQIITAAATPEKYLQFPHNLSNL 60
QY 61 DRIFDKTPEP 70
DB 170 ERIFDKTPEP 179

```

```

RESULT 11
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stoult, John T
; APPLICANT: Lau, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-838-151A-4

Query Match 59.3%; Score 214; DB 4; Length 361;
 Best Local Similarity 55.7%; Pred. No. 4e-21;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLWGEFVDGSRGGCOTSDNDAAEALNASSKEALQIIAAATPEKYLTFQFHNLSNL 60
 Db 110 TLWGEFVDGSRGGCOTSDNDAAEALNASSKEALQIIAAATPEKYLTFQFHNLSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 170 ERIFAKAPEP 179

RESULT 12
 US-08-838-151A-6

; Sequence 6; Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATE: Release #1.0, Version #1.30
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-838-151A-6

Query Match 59.3%; Score 214; DB 4; Length 361;
 Best Local Similarity 55.7%; Pred. No. 4e-21;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLWGEFVDGSRGGCOTSDNDAAEALNASSKEALQIIAAATPEKYLTFQFHNLSNL 60
 Db 110 TLWGEFVDGSRGGCOTSDNDAAEALNASSKEALQIIAAATPEKYLTFQFHNLSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 170 ERIFAKAPEP 179

RESULT 13
 US-08-838-151A-8

; Sequence 6; Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATE: Release #1.0, Version #1.30
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-838-151A-8

Query Match 59.3%; Score 214; DB 4; Length 361;
 Best Local Similarity 55.7%; Pred. No. 4e-21;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLWGEFVDGSRGGCOTSDNDAAEALNASSKEALQIIAAATPEKYLTFQFHNLSNL 60
 Db 110 TLWGEFVDGSRGGCOTSDNDAAEALNASSKEALQIIAAATPEKYLTFQFHNLSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 170 ERIFAKAPEP 179

RESULT 14

US-08-838-151A-24
 ; Sequence 24; Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rockey, Milnamow & Katz
 CITY: Chicago
 STREET: Two Prudential Plaza, Suite 4700
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/838,151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/POCKET NUMBER: SVS3801P0260
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-838-151A-24

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 Best Local Similarity 63.9%; Pred. No. 3.2e-19;
 Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
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 Db 111 FGVSDIGSRGSGQSQANDAYAEALNNGSGKSEALNLKEKAPKDYILQFHNLSNLDRI 170
 Qy 64 F 64
 Db 171 F 171

RESULT 15
 US-08-838-151A-27
 : Sequence 27, Application US/08838151A
 : Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hong
 APPLICANT: Douglas
 APPLICANT: Ahquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Gcmminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rockey, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/838,151A
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/POCKET NUMBER: SVS3801P0260
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-838-151A-27
 Query Match 55.4%; Score 200; DB 4; Length 357;
 Best Local Similarity 63.9%; Pred. No. 3.2e-19;
 Matches 39; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
 Qy 4 WEEVDGSRGSGCOPTSDAAAFALNASSKSEALQITAAATPEKYLQFHNLSNLDRI 63
 Db 111 FGVSDIGSRGSGQSQANDAYAEALNNGSGKSEALNLKEKAPKDYILQFHNLSNLDRI 170
 Qy 64 F 64
 Db 171 F 171
 Search completed: January 3, 2002, 15:38:49
 Job time: 226 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.
 OW protein - protein search, using sw model
 Run on: January 3, 2002, 15:37:37 : Search time 144.17 Seconds
 (without alignments)
 35,965 Million cell updates/sec

Title: us-09-289-346a-5
 Perfect score: 359
 Sequence: 1 TLVWGFQVDSARGCQTPQPHNLNLDRIEDTPEP 70

Scoring table:
 BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 52463 seqs, 7407390 residues
 Total number of hits satisfying chosen parameters: 52463

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Maximum Match 0%

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 22: /SID58/gcgdata/genescq/genescq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	359	100.0	70	21	AA18681	Mutant peptide der
2	343	95.5	70	21	AA18677	Peptide fragment f
3	343	95.5	356	21	AA18687	Amino acid sequenc
5	335	93.3	70	21	AA18685	Mutant peptide der
6	331	92.2	70	21	AA18692	Mutant peptide der
7	329	91.5	70	21	AA18684	Mutant peptide der
8	329	91.6	70	21	AA18690	Mutant peptide der
9	328	91.4	70	21	AA18678	Mutant peptide der
10	328	91.4	70	21	AA18686	Mutant peptide der
11	327	91.1	70	21	AA18689	Mutant peptide der

12	325	90.5	70	21	AA18680	Mutant peptide der
13	325	90.5	70	21	AA18691	Mutant peptide der
14	321	89.4	70	21	AA18683	Mutant peptide der
15	319	88.9	70	21	AA18693	Mutant peptide der
16	313	86.9	70	21	AA18692	Mutant peptide der
17	220	61.3	361	18	AAW34326	Tomato mottle viru
18	220	61.3	361	18	AAW34324	Tomato mottle viru
19	220	61.3	361	18	AAW34325	Tomato mottle viru
20	220	61.3	361	18	AAW34326	Tomato mottle viru
21	219	61.0	359	17	AAW88870	Sardinian tomato y
22	219	61.0	359	17	AAW88871	Sardinian tomato y
23	218	60.7	353	18	AAW34328	Sardinian tomato y
24	218	60.7	353	18	AAW34328	Bean golden mosaic
25	218	60.7	353	18	AAW34332	Bean golden mosaic
26	218	60.7	353	18	AAW34333	Bean golden mosaic
27	218	60.7	353	18	AAW34334	Bean golden mosaic
28	218	60.7	353	18	AAW34335	Bean golden mosaic
29	216	60.2	353	8	AAW70407	ORF 4, gene product
30	208.5	58.1	361	8	AAW70562	Phytochrome A
31	203	56.5	357	18	AAW34329	Tomato yellow leaf
32	203	56.5	357	18	AAW34329	Tomato yellow leaf
33	203	56.5	357	18	AAW34330	Tomato yellow leaf
34	203	56.5	357	18	AAW34331	Tomato yellow leaf
35	195	54.3	357	18	AAW68473	Tomato yellow leaf
36	66.5	18.5	512	19	AAW68473	Tomato yellow leaf
37	63.5	17.7	1693	21	AAW84857	HIV-1 strain YBF30
38	63.5	17.7	1693	21	AAW84859	Human laminin 5 po
39	63.5	17.7	1693	21	AAW84860	Reduced sequence o
40	63.5	17.7	1713	21	AAW84858	Human laminin 5 po
41	63.5	17.7	1713	21	AAW84858	Human laminin 5 po
42	60.5	16.9	131	18	AAW34327	Tomato mottle viru
43	60.5	16.9	447	21	AAW96659	Human GTPase assoc
44	60.5	16.9	447	21	AAW87089	Human secreted pro
45	60.5	16.9	447	22	AAW65267	Human PRO1125 (UNQ

ALIGNMENTS

RESULT 1
 AAB18681
 ID AAB18681 standard; peptide; 70 AA.
 XX
 XX AAB18691;
 DT 22-JAN-2001 {first entry}
 XX
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
 XX
 XX Geminivirus: replication protein; Rep protein; All; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS
 OS Tomato golden mosaic virus.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 47
 FT Misc-difference 48 /note= "wild type residue replaced with Ala"
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"
 FT
 XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000: 2000WO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 XX 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX DR WPI: 2000-618851/59.
 XX PI Transgenic plants with increased resistance to geminivirus infection
 XX PT comprise a nucleic acid construct containing a nucleic acid sequence
 XX PT encoding a mutant A11 protein with a mutation in the RB binding region
 XX PT .
 XX PS Claim 52: Page 44; 73pp; English.
 XX CC The present sequence represents a mutant peptide, derived from a
 XX CC geminivirus replication (rep) protein, also known as A11. A11 binds
 XX CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 XX CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 XX CC protein are used to produce transgenic plants. The mutation in A11 is
 XX CC present in a ribosome binding region, and expression of mutant A11
 XX CC protein imparts increased resistance to geminivirus infection in the
 XX CC transgenic plants. The present sequence represents a mutant A11 protein
 XX CC possessing resistance to geminivirus infection in the transgenic plants.
 XX CC Tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 XX CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 XX CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 XX CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 XX CC virus, cotton leaf curl virus or beet curly top virus.
 XX SQ Sequence 70 AA:
 Query Match 100.0%; Score 359; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 2.5e-39;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLVGEFQVDCRGAGCGCOTSDAAAEALNASKEEALQITREKTPAALFQPHNLSNL 60
 DB 1 TLVGEFQVDCRGAGCGCOTSDAAAEALNASKEEALQITREKTPAALFQPHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 drifdktp 70
 RESULT 2
 ID AAB18677 standard; peptide: 70 AA.
 AC AAB18677;
 DT 22-JAN-2001 (first entry)
 DE XX Peptide fragment from Rep protein of TGMV (amino acids 110-179).
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 OS Tomato golden mosaic virus.
 XX WO2000054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the RB binding region
 PT .
 PT Disclosure: Page 18; 73pp; English.
 XX CC The present sequence is derived from a geminivirus replication (Rep)
 XX CC protein, which is also known as A11. A11 binds double-stranded DNA,
 XX CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 XX CC with other viral and host proteins. Mutants of the A11 protein are used
 XX CC to produce transgenic plants. The mutation in A11 is present in a
 XX CC ribosome binding region, and expression of mutant A11 protein in a
 XX CC plant imparts increased resistance to geminivirus infection in the plant. Mutant A11
 XX CC proteins are useful for producing plants having increased resistance or
 XX CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 XX CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 XX CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 XX CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 XX CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 XX CC beet curly top virus.
 XX SQ Sequence 70 AA:
 Query Match 95.5%; Score 343; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 3e-37;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TLVGEFQVDCRGAGCGCOTSDAAAEALNASKEEALQITREKTPAALFQPHNLSNL 60
 DB 1 TLVGEFQVDCRGAGCGCOTSDAAAEALNASKEEALQITREKTPAALFQPHNLSNL 60
 QY 61 DRIFDKTPEP 70
 DB 61 drifdktp 70
 RESULT 3
 ID AAB18687 standard; peptide: 356 AA.
 AC AAB18687;
 DT 22-JAN-2001 (first entry)
 DE XX Amino acid sequence of a geminivirus replication protein of TGMV.
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 OS Tomato golden mosaic virus.
 XX WO2000054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 XX 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 XX
 PS Disclosure: Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 CC Sequence 70 AA:

Query Match 92.5%; Score 332; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 8.2e-36;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWCEFDVGRSGCGTSDNAAAEALNASKEEALQIIREKIPAAALQFHNHNSNL 60
 DB 1 TLVWGFQVGRSGCGTSDNAAAEALNASKEEALQIIREKIPAAALQFHNHNSNL 60
 QY 61 DRFDKTPPEP 70
 DB 61 drfdktppep 70

RESULT 6
 ID AAB18692 standard; peptide: 70 AA.
 XX AAB18692;
 XX

DT 22-JAN-2001 (first entry)
 XX

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 XX

OS Synthetic.
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"
 FT Misc-difference 64 /note= "wild type residue replaced with Ala"

FT WO200054573-A1.
 XX

XX 21-SEP-2000.
 XX

XX 15-MAR-2000; 2000MO-US06759.
 XX

XX 18-MAR-1999; 99US-0125004.
 PR

XX 09-APR-1999; 99US-0289346.
 PR

XX (UYN-) UNIV NORTH CAROLINA STATE.
 XX

XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI

XX WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 XX
 PS Disclosure: Page 50; 73pp; English.
 XX

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX

Sequence 70 AA:

Query Match 92.2%; Score 331; DB 21; Length 70;
 Best Local Similarity 92.2%; Pred. No. 1.2e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWCEFDVGRSGCGTSDNAAAEALNASKEEALQIIREKIPAAALQFHNHNSNL 60
 DB 1 TLVWGFQVGRSGCGTSDNAAAEALNASKEEALQIIREKIPAAALQFHNHNSNL 60
 QY 61 DRFDKTPPEP 70
 DB 61 drfdktppep 70

RESULT 7
 ID AAB18684 standard; peptide: 70 AA.
 XX AAB18684;
 XX

DT 22-JAN-2001 (first entry)
 XX

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 XX

OS Synthetic.
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FT Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"
 FT Misc-difference 64 /note= "wild type residue replaced with Ala"

FT WO200054573-A1.
 XX

XX 21-SEP-2000.
 XX

XX 15-MAR-2000; 2000MO-US06759.
 XX

XX 18-MAR-1999; 99US-0125004.
 PR

XX 09-APR-1999; 99US-0289346.
 PR

XX (UYN-) UNIV NORTH CAROLINA STATE.
 XX

(UYNC-) UNIV NORTH CAROLINA STATE.
Hanley-Bowdoin L, Orozco BM, Kong L;
WPI: 2000-618851/59.

Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region

Claim 52; Page 45; 73pp; English.

The present sequence represents a mutant peptide, derived from a double-stranded DNA catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a ribosome binding region, and expression of mutant A11 protein imparts increased resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, African cassava mosaic virus, Indian virus, tomato leaf curl virus, African cassava mosaic virus, bean curly cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA:

Query Match 91.6%; Score 329; DB 21; Length 70;
Best Local Similarity 92.9%; Pred.No. 2e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLVWGEPQVDGRSGAGCGCOTSDNDAAEALNASKEEALQLIREKIPAAALFQPHNLNSL 60
DB 1 TLVWGAADVGRSGAGCGCQTSDNDAAEAALNASKEEALQLIREKIPAAALFQPHNLNSL 60
OY 61 DRIFDKTPEP 70
DB 61 drifdktppep 70

RESULT 8
AAB18690 standard; peptide: 70 AA.
ID AAB18690
AC AAB18690;
XX 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (ALL) protein.
DE Geminivirus: replication protein; Rep protein; A11; transgenic plant;
KW ribosome binding region; resistance; geminivirus infection.
OS Synthetic.
XX Tomato golden mosaic virus.
OS Location/Qualifiers
FH Misc-difference 27 /note= "wild type residue replaced with Ala"
FT FT
FT Misc-difference 30 /note= "wild type residue replaced with Ala"
FT FT
FT Misc-difference 31 /note= "wild type residue replaced with Ala"
FT FT
FT W0200054573-A1.
PN 21-SEP-2000.
PD 15-MAR-2000; 2000MO-US06759.
XX 18-MAR-1999; 99US-0125004.
XX 09-APR-1999; 99US-0289346.

OS Tomato golden mosaic virus.
 FH Key Location/Qualifiers
 FT Misc-difference 34 /note= "wild type residue replaced with Ala"
 FT Misc-difference 35 /note= "wild type residue replaced with Ala"
 FT Misc-difference 36 /note= "wild type residue replaced with Ala"
 FT
 FT
 PN WO200054573-A1.
 XD 21-SEP-2000.
 XX
 XX
 PF 15-MAR-2000; 2000MO-US06759.
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT
 XX Disclosure: Page 49: 73pp: English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance to geminivirus infection in the
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX Sequence 70 AA;
 SQ
 Query Match 90.5%; Score 325; DB 21: Length 70;
 Best Local Similarity 91.4%; Pred. No. 6.7e-35;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 TLVGEFVDFGRGAGCGCTSDNAAEALNASSKEAFQIIRKIPAAALQPHNINSL 60
 DB 1 TLVGEFVDFGRGAGCGCTSDNAAEALNASSKEAFQIIRKIPAAALQPHNINSL 60
 OY 61 DRIFDKTPEP 70
 DB 61 drifdktp 70
 RESULT 14
 AAB18683
 XX AAB18683 standard; peptide: 70 AA.
 AC AAB18683;
 DT 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX

KW Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 OS Tomato golden mosaic virus.
 FT Key Location/Qualifiers
 FT Misc-difference 59 /note= "wild type residue replaced with Ala"
 FT Misc-difference 61 /note= "wild type residue replaced with Ala"
 FT Misc-difference 62 /note= "wild type residue replaced with Ala"
 FT
 PN WO200054573-A1.
 XD 21-SEP-2000.
 XX
 XX
 PF 15-MAR-2000; 2000MO-US06759.
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT
 XX Claim 53: Page 45: 73pp: English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX Sequence 70 AA;
 SQ
 Query Match 89.4%; Score 321; DB 21: Length 70;
 Best Local Similarity 91.4%; Pred. No. 2.2e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 TLVGEFVDFGRGAGCGCTSDNAAEALNASSKEAFQIIRKIPAAALQPHNINSL 60
 DB 1 TLVGEFVDFGRGAGCGCTSDNAAEALNASSKEAFQIIRKIPAAALQPHNINSL 60
 OY 61 DRIFDKTPEP 70
 DB 61 aalifdktp 70
 RESULT 15
 AAB18682
 ID AAB18682 standard; peptide: 70 AA.
 AC AAB18682;
 XX

Job time: 154 sec

DT 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
 KW Geminivirus: replication protein; Rep protein; All; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 OS Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 FH Note- "wild type residue replaced with Ala"
 FT Misc-difference 54
 FT Note- "wild type residue replaced with Ala"
 FT Misc-difference 55
 FT Note- "wild type residue replaced with Ala"
 XX
 XX W0200054573-Al.
 FN
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI
 XX
 XX WPI: 2000-618851/59.
 DR
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant All protein with a mutation in the N0 binding region
 PT
 XX
 XX Claim 53; Page 44-45; 73pp: English.
 PS
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as All. All binds
 CC DNA's stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA's, and is used to produce transgenic plants. The mutation in All
 CC protein is in a ribosome binding region, and expression of mutant All
 CC present in a ribosome binding region, and expression of mutant All
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant All proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf
 CC curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA:
 SQ
 Query Match 88.98; Score 319; DB 21; Length 70;
 Best Local Similarity 91.48; Pred No 4, 1e-34;
 Matches 64; Conservative 0; Mismatches 0; Gaps 0;
 Oy 1 TLVGEFQVDRSARGCQTSNDAAALNASSKEALQTIREFTPAAALFQFHNLSNL 60
 Db 1 TLVGEFQVDRSARGCQTSNDAAALNASSKEALQTIREFTPAAALFQFHNLSNL 60
 Oy 61 DRIDKTPPEP 70
 Db 61 DRIDKTPPEP 70

Search completed: January 3, 2002, 15:37:37

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:09 : Search time 72.75 Seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346a-5
Search score: 90
Sequence: 1 TLWGEFQVDSARGCQT.....FQFNLSNLRIDFKTPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
maximum match of the same length as the query, assuming a random
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343	95.5	352	1 QOCVLT	ALI protein - tota
2	247	68.8	361	1 QOCVPT	ALI protein - tota
3	243	67.7	358	2 J07584	hypothetical prote
4	232	64.6	362	1 J01887	ALI protein - tota
5	226	63.0	359	2 S32211	gene C1 protein -
6	224	62.4	349	2 JQ3211	replicase - pepper
7	219	62.0	359	2 JQ3203	ALI protein - pep
8	219	62.0	359	2 S22503	ALI protein - pep
9	216	60.2	351	2 JQ2327	ALI protein - tota
10	216	60.2	358	1 J01870	ALI protein - tota
11	215	59.9	355	1 QOCVW1	gene C1 protein -
12	213	59.3	359	2 S32235	ALI protein - beet
13	212	59.1	385	2 S28360	replication-associ
14	209	58.2	360	2 S59855	ALI protein - tota
15	208	57.3	360	2 S59855	ALI protein - tota
16	194	56.3	331	2 S50559	ALI protein - tota
17	118	32.9	347	1 QOCV31	ALI protein - tota
18	65	18.1	587	2 JQ3149	FC gamma (IgG) rec
19	63.5	17.7	1713	2 A55347	adhesive ligand ep
20	62	17.3	160	2 G82060	protein maturation
21	62	17.3	368	2 E86840	E1 protein - human
22	61	17.0	312	2 S35505	Probable large ATP
23	60.5	16.9	439	2 A33142	hypothetical prote
24	60.5	16.9	439	2 E59036	hypothetical prote
25	60.5	16.9	447	2 T12544	1-phosphatidylinos
26	60.5	16.9	447	2 A54600	probable NADH oxid
27	60.5	16.9	1070	1 A54600	probable NADH oxid
28	60	16.7	396	2 B71078	hypothetical prote
29	59.5	16.6	707	2 H71077	hypothetical prote

30 59.5 16.6 1053 2 T06483
31 59.5 16.6 1610 2 A46227
32 59.5 16.6 1646 2 JH0242
33 59.5 16.6 2137 2 T05244
34 59.5 16.6 2181 2 JH0156
35 59.5 16.6 2181 2 A46156
36 59.5 16.6 2203 2 T42742
37 59 16.4 751 2 S26839
38 59 16.4 403 2 A33362
39 59 16.4 1852 2 A37860
40 58.5 16.3 388 2 C62196
41 58 16.2 1988 2 P86316
42 58 16.2 1245 2 S83110
43 58 16.2 1245 2 S83110
44 58 16.2 1341 2 JG0166
45 58 16.2 1608 2 A28182

probable ubiquitin
voltage-dependent
hypothetical prote
calcium channel al
voltage-dependent
retrovirus-related
UDP-glucose--glyco
calcium channel pr
hypothetical prote
protein T10022.13
hypothetical prote
voltage-dependent
LAMP1 protein - L
hemolysin A - Serr

ALIGNMENTS

RESULT 1
QOCVLT
ALI protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #text-change 08-Apr-1994
C:Accession: A04170 Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBL: J01887, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Residues: 1-352 <HAM>
C:Map position: segment A
C:Genetics:
C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 95.5% Score 343; DB 1; Length 352;
Best Local Similarity 95.7% Pred. No. 1:7e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSARGCQTSNDAAAEALNASSKEEALQIREKIPAAALFQFNLSNLSL 60
|||||
DB 111 TLWGEFQVDSARGCQTSNDAAAEALNASSKEEALQIREKIPKTYLFQFNLSNLSL 170
|||||

QY 61 DRIFUKTPEP 70
|||||
DB 171 DRIFUKTPEP 180
|||||

RESULT 2
QOCVPT
ALI protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
A:Note: June 1992 #sequence-revision 30-Jun-1992 #text-change 16-Jun-2000
C:Accession: J00364 Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
R:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; MUID:91311403
A:Accession: J00364
A:Status: translation not shown
A:Residues: 1-161
A:Molecule type: DNA
A:Reference number: J00362; MUID:91311403
C:Cross-references: GB:D00940; NID:9222458; PIDN:BAA00782.1; PID:9222459
C:Genetics:
C:Map position: segment A
C:Superfamily: tomato golden mosaic virus ALI protein

```
Df      110 TLEWGFQVDGRSARGGQSNDAYAAQLNTGSKEALNWRELAKPDVLOFHNLNSL 69  

QY       GI DRI-----FDKTPF 69  

         IIII  

Db      170 DRIFTPLPVIVVSFLSSSFDRPFE 194  

        -----  

RESULT    5  

gene C1 protein - tomato yellow leaf curl virus  

C:Species: tomato yellow leaf curl virus  

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999  

CAccession: S39211  

submitted to the EMBL Data Library, August 1993  

R:Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.  

A:Accession number: S39209  

A:Reference number: S39208  

A:Accession: S39211  

A>Status: preliminary  

A:Molecule type: DNA  

A:Residues: 1-359 <NOR>  

A:Cross-references: EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g433658  

C:Superfamily: tomato golden mosaic virus AL1 protein
```

```
Query Match          63.0%; Score 226; DB 2; Length 359;  
Best Local Similarity 60.9%; Pred. No. 3.8e+18;  
Matches 42; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
```

```
QY      2 LWMGFFGVDRSGRGCGTSDNAAEALNASKEEALQIIIRKIPAAAFQHNLNSMLD 61  
         |||||.....|||||..|||...|||....|||...|||...|||...|||...|||...|||..  
Db     111 LEWGFIQDSARGGGQTANDARAKNNASKEADVLRELLARYLIIMFINSLMD 170  
         .....|||.....|.....|.....|.....|.....|.....|.....|.....|.....|..  
QY     62 RIDEKTPEP 70  
         I:I : | | |  
Db    171 RVFOQPAP 179  
         ..:::  
RESULT    6  
replicase - pepper huasteco virus (component A)  
NAlternate names: ORF Al1 protein  
C:Species: pepper huasteco virus  
C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Sep-1999  
CAccession: J02300  
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estralla, L.; Rivera-Bustamante,  
A.; Gen. Virol., 1994, 74, 2225-2231, 1993  
A:Status: preliminary  
A:Reference number: J02299; MUTD:S94U15007  
A:Accession: J02300  
A:Molecule type: DNA  
A:Residues: 1-349 <TOR>  
A:Cross-references: GB:J70418; NID:g61023; PIDN:CAA9856.1; PID:g61025  
C:Superfamily: tomato golden mosaic virus AL1 protein
```

```
Query Match          62.4%; Score 224; DB 2; Length 349;  
Best Local Similarity 61.4%; Pred. No. 6.2e+18;  
Matches 43; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
```

```
OY      1 TLWGEFGVDGRSARGGCTSDNAEAALNASKEEALQIIIRKIPAAAFQHNLNSL 60  
         ::::::::::::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||..  
Db     110 TWVGDFIQDSARGGQSNDOTFAKANSAEEALQIIDEPJOHFFLFPHNYISNA 169  
         .....|||.....|.....|.....|.....|.....|.....|.....|.....|.....|..  
OY     61 DRIFDKTEP 70  
         :||| : |||  
Db    170 NRIFOPTPEP 179  
         ....:
```

```
RESULT    7  
Al1 protein - pepper rizado amarillo virus  
C:Species: pepper rizado amarillo virus
```

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 20-Sep-1999
 C:Accession: S31875
 R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-Buonafina, P.; et al. 1995. Complete nucleotide sequence of pepper huasteco virus and comparison with the EMBL Data Library, February 1993
 A:Description: Complete nucleotide sequence of pepper huasteco virus
 A:Accession: S31875
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <TOR>
 A:Cross-references: EMBL:X70418; NID:g61023; PIDN:CA94856.1; PID:g61025
 A:Note: the source is designated as pepper huasteco virus
 C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 62.4%; Score 224; DB 2; Length 349;
 Best Local Similarity 61.4%; Pred. No. 6.2e-18;
 Matches 43; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLWGTFQVGRSARGCGTSDNDAAEALNASSKEEALQIIRKIPAAALFOFINLNSLND 60
 Db 110 TVWGEFQIDGRSARGCGSANDYAKALNAGSKAEALQIIRKIPAAALFOFINLNSLND 169

Qy 61 DRIFDKTPEP 70
 Db 170 NRIFOTPEP 179

RESULT 8
 S22593
 hypothetical protein C4 - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
 C:Accession: S22593
 R:Kheyr-Pour, A.; Bendahmane, M.; Watzelt, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.; et al. 1995. Complete nucleotide sequence of tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite virus
 A:Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite virus
 A:Reference number: S22588; MUID:92107660
 A:Accession: S22593
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-359 <RHE>
 A:Cross-references: EMBL:X61153; NID:g62211; PIDN:CA94366.1; PID:g62217
 A:Note: the source is designated as tomato golden mosaic virus ALL protein
 C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 61.0%; Score 219; DB 2; Length 359;
 Best Local Similarity 58.0%; Pred. No. 2.4e-17;
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 2 TLWGTFQVGRSARGCGTSDNDAAEALNASSKEEALQIIRKIPAAALFOFINLNSLND 61
 Db 111 LWGTFQIDGRSARGCGTSDNDAAEALNAGSKAEALQIIRKIPAAALFOFINLNSLND 170

Qy 62 RIFKOTPEP 70
 Db 171 KVFQVPAP 179

RESULT 9
 JQ2327
 All protein - Indian cassava mosaic virus
 R:Alternate names: replication-associated protein
 C:Species: Indian cassava mosaic virus
 C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
 R:Homestead, Y.C.; Robinson, B.D.; Harrison, B.D.
 J. Gen. Virol. 74, 2437-2443, 1993
 A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted strains of the replication-associated protein of the Indian cassava mosaic virus
 A:Reference number: JQ2326; MUID:94065670
 A:Accession: JQ2327
 A:Molecule type: DNA

A:Residues: 1-351 <HON>
 A:Cross-references: EMBL:Z24758; NID:g395351; PIDN:CA90891.1; PID:g584046
 C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 60.2%; Score 216; DB 2; Length 351;
 Best Local Similarity 62.7%; Pred. No. 5.1e-17;
 Matches 42; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 4 WGEFQVGRSARGCGTSDNDAAEALNASSKEEALQIIRKIPAAALFOFINLNSLND 63
 Db 113 WGTDFQIDGRSARGCGSANDYAKALNAGSKAEALQIIRKIPAAALFOFINLNSLND 172

Qy 64 FDKTPEP 70
 Db 173 FTKPEP 179

RESULT 10
 JQ1870
 coat protein - tomato mottle virus (isolate Florida)
 C:Species: tomato mottle virus
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
 C:Accession: JQ1870
 R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.
 J. Gen. Virol. 73, 3225-3229, 1992
 A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from tomato
 A:Reference number: JQ1869; MUID:93107858
 A:Accession: JQ1870
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-358 <ABO>
 A:Cross-references: GB:L14460
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 60.2%; Score 216; DB 1; Length 358;
 Best Local Similarity 57.1%; Pred. No. 5.2e-17;
 Matches 40; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 1 TLWGTFQVGRSARGCGTSDNDAAEALNASSKEEALQIIRKIPAAALFOFINLNSLND 60
 Db 107 TIWGFQIDGRSARGCGSANDYAKALNAGSKAEALQIIRKIPAAALFOFINLNSLND 166

Qy 61 DRIFDKTPEP 70
 Db 167 ERIFAKPEP 176

RESULT 11
 CCQVMI
 AV1 protein - abutilon mosaic virus (isolate West India)
 C:Species: abutilon mosaic virus
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
 R:Friscimuth, T.; Zimmat, G.; Jeske, H.
 Virol. 70, 461-469, 1990
 A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as well as eukaryotic features
 A:Reference number: A36214; MUID:91020984
 A:Accession: A36214
 A:Molecule type: DNA
 A:Residues: 1-355 <FRI>
 A:Cross-references: EMBL:X15983
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 59.9%; Score 215; DB 1; Length 355;
 Best Local Similarity 58.5%; Pred. No. 6.7e-17;
 Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

```

Oy 1 TLVMEFQVDSRGSGCOTSDNAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60
   I : |||||:|||||:||||:||||:| : |||:| : | : |||:|
Db 110 TAEFGFQIDGSRGSGQOTANDSTAKALAGDWSALNLTKEQPKDYVLQNHTRSNL 169
   Qy 61 DRIFDKTPRP 70
   |||||:|||||
Db 170 ERIFAKADPE 179
   |||||:|||||

RESULT 12
gene Cl protein- tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Accession: S39235
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
R:Creptl, S.; Noris, A.; Bosco, D.; Accotto, G.
submitted to the EMBL Data Library, December 1993
A:Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.
A:Reference number: S39233
A:Accession: S39235
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <CRE>
A:Cross-references: EMBL:Z28390; NID:q1041671; PID:g1334964
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.3%; Score 213; DB 2; Length 359;
Best Local Similarity 55.7%; Pred. No. 1.6e-16;
Matches 39; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Oy 2 LVWGEFQVDSRGSGCOTSDNAAEALNASSKEALQIREKIPAAALFQFHNLSNL 61
   I : |||||:|||||:||||:||||:| : |||:| : | : |||:|
Db 111 LEMGTQIDGSRGSGQOTANDAYAKANARKSEALDYKQLAPROYLHFHNISNLD 170
   Qy 62 RIFDKTPRP 70
   |||||:|||||
Db 171 KVFQVPPAP 179
   |||||:|||||

RESULT 13
Z28360 protein- beet curly top virus
C:Species: beet curly top virus
C:Date: 07-May-1991 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
R:Stanley, J.; Markham, P.G.; Callis, R.J.; Pinner, M.S.
EMBO J. 5, 1761-1767, 1986
A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top
A:Reference number: Z28360
A:Accession: Z28360
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-385 <STA>
A:Cross-references: GB:M24597; EMBL:X04144; NID:g210678; PIDN:AAA42751.1; PID:g210679
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 59.1%; Score 212; DB 2; Length 365;
Best Local Similarity 55.7%; Pred. No. 1.6e-16;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLVMEFQVDSRGSGCOTSDNAAEALNASSKEALQIREKIPAAALFQFHNLSNL 60
   I : |||||:|||||:||||:||||:| : |||:| : | : |||:|
Db 137 TIEGFEQIDGSRGSGQOTANDSTAKALNTSDQNLTKKEQPKDYFLQHNLINNA 196
   Qy 61 DRIFDKTPRP 70
   |||||:|||||
Db 197 QKIFQRPDP 206
   |||||:|||||

RESULT 14

```

```

S59885
replication-associated protein Cl - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: S59885
R:Hong, J.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A:Description: Nucleotide sequences from tomato leaf curl viruses from different coun
d geminiviruses.
A:Reference number: S58346
A:Accession: S59885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-360 <HNS>
A:Cross-references: EMBL:Z48182; NID:q944839; PIDN:CAA89229.1; PID:q974211
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 58.2%; Score 209; DB 2; Length 360;
Best Local Similarity 62.1%; Pred. No. 3.3e-16;
Matches 41; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Oy 4 WGEFQVDSRGSGCOTSDNAAEALNASSKEALQIREKIPAAALFQFHNLSNL 63
   I : |||||:|||||:||||:||||:| : |||:| : | : |||:|
Db 113 FGVFQIDGSRGSGCOTANDAYAEALNASSKEALDILREKAPKDYVLFQFHNLSNLDRI 172
   Qy 64 FUKTPE 69
   |||||:|||||
Db 173 FFPSPS 178
   |||||:|||||

RESULT 15
QOCVCI
AL1 protein - tomato yellow leaf curl virus
N:Alternate names: Cl protein
C:Species: tomato yellow leaf curl virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A:Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a sin
A:Reference number: A40779; NID:92024070
A:Accession: D40779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <NAV>
A:Cross-references: NID:X15656; NID:q62204; PIDN:CAA33688.1; PID:g62207
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match 56.5%; Score 203; DB 1; Length 357;
Best Local Similarity 64.4%; Pred. No. 1.6e-15;
Matches 40; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Oy 4 WGEFQVDSRGSGCOTSDNAAEALNASSKEALQIREKIPAAALFQFHNLSNL 63
   I : |||||:|||||:||||:||||:| : |||:| : | : |||:|
Db 111 FVQSQIDGSRGSGCOTANDAYAEALNASSKEALNLTKEKAPKDYILOFINLSNLDRI 170
   Qy 64 F 64
   |||||:|||||
Db 171 F 171
   |||||:|||||

Search completed: January 3, 2002, 15:40:10
Job time: 306 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:57:15 : Search time 43.68 Seconds
(Without alignments)
58.758 Million cell updates/sec

Title: US-09-289-346a-5
Perfect score: 359
Sequence: 1 TLWGEFQVDRSARGGCGT.....FOEILNSLDRFDKTEP 70

Scoring table: BLOSUM62

Gapop 10.0, , Dextp 0.5

Searched: 100059 seqs, 36564827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	95.5	352	1 VAL1_TGMV	P03567 tomato gold
2	247	68.9	361	1 VAL1_PYRV	P27258 potato yell
3	247	68.9	361	1 VAL1_PYRV	P27258 potato yell
4	243	67.7	358	1 VAL1_CLVN	P14572 cassava lat
5	232	64.6	362	1 VAL1_TYLCV	P36279 tomato yell
6	226	63.0	359	1 VAL1_TYLCV	P36609 tomato yell
7	224	62.4	349	1 VAL1_PYRV	P06923 pepper hus
8	219	61.0	359	1 VAL1_TYLCV	P27260 tomato yell
9	216	60.2	353	1 VAL1_TGMV	P05175 bean golden
10	216	59.4	355	1 VAL1_PYRV	P06627 tomato mott
11	211	59.2	355	1 VAL1_PYRV	P06627 tomato mott
12	212	59.1	358	1 VAL1_PYRV	P14591 beet curly
13	203	56.5	357	1 VAL1_TYLCV	P27259 tomato yell
14	118	32.9	347	1 VAL1_SICV	P29048 squash leaf
15	65	18.1	630	1 VEL_HPV66	P01687 human papil
16	63.5	17.7	1713	1 LMA3_HDMAN	P06787 homo sapien
17	62.5	17.4	428	1 GBA_CRYAL	P28668 candida alb
18	61.5	17.0	428	1 GBA_CRYAL	P28668 candida alb
19	60.5	16.9	447	1 TBL2_HUMAN	P09403 homo sapien
20	60.5	16.9	1070	1 P11B_HUMAN	P42238 homo sapien
21	59.5	16.6	706	1 Y006_RTCPR	P09266 rickettsia
22	59.5	16.6	1053	1 UBA3_WHEAT	P31252 triticum ae
23	59.5	16.6	1610	1 QAD4_MESAU	P09244 mesocricetu
24	59.5	16.6	2161	1 CCAD_HUMAN	P01658 homo sapien
25	59.5	16.6	2161	1 CCAD_HUMAN	P01658 homo sapien
26	59.5	16.6	2703	1 GSD_RAT	P27732 rattus norv
27	59.5	16.6	2703	1 GSD_RAT	P27732 rattus norv
28	59.5	16.6	1852	1 CCAS_CYPCA	P22316 cyprinus car
29	58	16.2	387	1 Y4PF_RHISN	P55615 thizobium s
30	58	16.2	1127	1 Y855_TREPA	O83827 treponema s
31	57.5	16.0	1608	1 HLVA_SERMA	P15320 seratia ma
32	57.5	16.0	367	1 LH4_MOUSE	P53776 mus musculu
33	57.5	16.0	511	1 HUTL_VIBCH	Q9ksq4 vibrio chol
34	57	15.9	355	1 CATE_RHOSH	P54905 rhodobacter

34 57 15.9 428 1 FUT1_MOUSE
35 57 15.9 432 1 PROA_DEIRA
36 57 15.9 432 1 PROA_DEIRA
37 57 15.9 432 1 PROA_DEIRA
38 57 15.9 874 1 SLAP_BACLI
39 56.5 15.7 1070 1 P11B_RAT
40 56 15.6 129 1 RK12_PORF
41 56 15.6 329 1 TC3A_CAEEL
42 56 15.6 427 1 FUT1_HUMAN
43 56 15.6 428 1 FUT1_RAT
44 55.5 15.5 265 1 E1FB_MICE
45 55.5 15.5 266 1 E1FB_MICE

ALIGNMENTS

RESULT 1
VAL1_TGMV
TO VAL1_TGMV STANDARD; PRT; 352 AA.
AC P03567:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALI PROTEIN.
GN AGL
OC tomato golden mosaic virus (TGMV)
CC NCBI TaxID=10831;
OX NCBI TaxID=10831;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamilton W.D.O., Stein V.E., Coutts R.H.A., Buck K.W.;
RT "Complete nucleotide sequence of the infectious cloned DNA components
of tomato golden mosaic virus: potential coding regions and regulatory
sequences. 2197-2205(1984).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALI PROTEIN FAMILY.
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CC EMBL; A02029; -; NOT_ANNOTATED_CDS.
DR PIR: A04170; Q0CV11.
DR InterPro: IPR001191; Gemin1_ALI.
DR Pfam: PF00799; Gemin1_ALI; 1.
DR PRINTS: PR00228; GEMCOATCLV1.
DR PRODOM: PD000736; Gemin1_ALI; 1.
KW NP-BIND.
FT AT-BOUND 223 230
FT ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 40332 MW; C33C938E5644B4A4 CRC64;

Query Match 95.5%; Score 343; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 2e-31;
Matches 67; Conservative 0; Mismatches 0; Gaps 0;

Cy 1 TLWGEFQVDRSARGGCGTSDNAAAEALNSKEEALQITREKIPAAALFOFHINSNL 60
Db 111 TLWGEFQVDRSARGGCGTSDNAAAEALNSKEEALQITREKIPKYLFOFHINSNL 170
Cy 61 DRIFDKTEP 70
Db 171 DRIFDKTEP 180

RESULT 2
VAL1_PYRV

ID VAL1_PMMV STANDARD; PRT: 361 AA.
 AC P27256;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 OS Potato yellow mosaic virus (isolate Venezuela).
 GS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10828;
 RN [1]
 RP MEDLINE=91311403; PubMed=1856690;
 RA MEDLINE=91311403; PubMed=1856690;
 RT "Potato yellow mosaic virus", Hamilton W.D.O.;
 RL J. Gen. Virol. 72:1515-1520(1991).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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 CC -----
 DR EMBL: D00940; IAA00782.1;
 DR IPIR: 003664; GEMINI_1;
 DR IPIR: 003664; GEMINI_1;
 DR Pfam: PF00799; Gemin1_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD000736; Gemin1_AL1.1.
 KM ATP-binding. 222 220 ATP (POTENTIAL).
 FT NP-BIND
 SQ SEQUENCE 361 AA; 40850 MW; 5627A3BF1264363 CRC64;

Query Match 68.8%; Score 247; DB 1; Length 361;
 Best Local Similarity 68.1%; Pred. No. 1.4e-20;
 Matches 47; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 Oy 1 TLVNGFQVDSARGCCTNDAAEAELMASKEALQIIRKIPAAALPQPHILNSNL 60
 Db 110 TLVNGFQVDSARGCCTNDAAEAELMASKEALQIIRKIPAAALPQPHILNSNL 169
 Oy 61 DRIEDKTPPE 69
 Db 170 DRIEMAPE 178

RESULT 3
 VAL1_CLVW STANDARD; PRT: 358 AA.
 ID VAL1_CLVW
 AC P14982;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 GN ACP1 PROTEIN (40.4 KDA PROTEIN).
 OS Cassava latent virus (strain West Kenyan 844).
 GS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stanley J., Gay M.R.;
 RT "Nucleotide sequence of cassava latent virus DNA";
 RL Nucleic Acids Res. 18:99-106(1990).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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 CC -----
 DR EMBL: J02057; NOT_GEMINIVIRUS;
 DR IPIR: 000000; GEMINI_1;
 DR Pfam: PF00799; Gemin1_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD00228; GEMCOATCLVL1.
 KM ATP-binding. 220 227 ATP (POTENTIAL).
 FT NP-BIND
 SQ SEQUENCE 358 AA; 40346 MW; ED15E73E92D569 CRC64;

Query Match 67.7%; Score 243; DB 1; Length 358;
 Best Local Similarity 64.3%; Pred. No. 3.8e-20;
 Matches 45; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 TLVNGFQVDSARGCCTNDAAEAELMASKEALQIIRKIPAAALPQPHILNSNL 60
 Db 109 TVENGFOIDGSRGCGQNDAYAKALNSGSALNWIHELVPDPVQLFHLNSNL 168
 Oy 61 DRIEDKTPPE 70
 Db 169 DRIETQPPAP 178

RESULT 4
 VAL1_CLVW STANDARD; PRT: 358 AA.
 ID VAL1_CLVW
 AC P14972;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 GN ACP1 PROTEIN (40.4 KDA PROTEIN).
 OS Cassava latent virus (strain Nigerian).
 GS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10819;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=2308431.
 RA Redington J., Richardson K., Eddy P.
 RT "Nucleotide sequence of the infectious cloned DNA components of
 RT African cassava mosaic virus (Nigerian strain).";
 RL Nucleic Acids Res. 18:197-198(1990).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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 CC -----
 DR EMBL: X17095; GMA34953.1;
 DR IPIR: S07594; S07594; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD00228; GEMCOATCLVL1.
 KM ATP-binding. 220 227 ATP (POTENTIAL).
 FT NP-BIND
 SQ SEQUENCE 358 AA; 40435 MW; IDB16B0CB2D5E2C CRC64;

Query Match 67.7%; Score 243; DB 1; Length 358;
 Best Local Similarity 64.3%; Pred. No. 3.8e-20;
 Matches 45; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 TLVNGFQVDSARGCCTNDAAEAELMASKEALQIIRKIPAAALPQPHILNSNL 60
 Db 109 TVENGFOIDGSRGCGQNDAYAKALNSGSALNWIHELVPDPVQLFHLNSNL 168
 Oy 61 DRIEDKTPPE 70
 Db 169 DRIETQPPAP 178

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QY 1 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 60
D 1 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 168
D 109 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 168
QY 61 DRIFDKTPEP 70
D 169 DRIFQPPAP 178

RESULT 5
ID VAL1:TYLVCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
OR Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=36447;
RN SEQUENCE FROM N.A.
RX MEDLINE=93139778; Pubmed=8423446;
RA Dry I.B., Ridgen J.E., Krake L.R., Mullineux P.M., Rezelian M.A.:
RA Nucleotide sequence and genome organization of tomato leaf curl
RA virus. J. Gen. Virol. 74:147-151(1993).
RL J. Gen. Virol. 74:147-151(1993).
RL -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
DR PIR: JQ1887; JQ1887.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCOTALL1.
DR PROSITE: PS00228; GEMCOTALL1.
DR ProDom: PD000736; Gemin1_AL1; 1.
KW ATP-binding. 221 228 ATP (POTENTIAL).
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B704058 CRC64;

Query Match 54.5%; Score 232; DB 1; Length 362;
Best Local Similarity 55.3%; Pred. No. 3.1e-18;
Matches 47; Conservative 8; Mismatches 14; Indels 16; Gaps 1;

QY 1 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 60
D 1 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 168
D 110 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 169
QY 61 DRI-----FQKTPG 69
D 170 DRIETPPVYVSPFLSSSEDRPVE 194

RESULT 6
ID VAL1:TYLVCU STANDARD; PRT; 359 AA.
AC P36279;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
OR Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=37139;
RN SEQUENCE FROM N.A.
RX MEDLINE=94256836; Pubmed=8198442;
RA Norris E., Hidalgo E., Accotto G., Moriones E.:
RA "High similarity among the tomato yellow leaf curl virus isolates
RA from the west Mediterranean basin: the nucleotide sequence of an
RA infectious clone from Spain.";

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Arch. Virol. 135:165-170(1994).
-1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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EMBL: Z25751; G4881026.1;
PIR: S39211; S39211.
InterPro: IPR001191; Gemin1_AL1.
Pfam: PF00799; Gemin1_AL1; 1.
PRINTS: PR00227; GEMCOTALL1.
PROSITE: PS00228; GEMCOTALL1.
ProDom: PD000736; Gemin1_AL1; 1.
ATP-binding. 221 228 ATP (POTENTIAL).
SEQUENCE 359 AA; 41065 MW; 2D170A51EF80A3EC CRC64;

Query Match 53.0%; Score 226; DB 1; Length 359;
Best Local Similarity 60.9%; Pred. No. 3.1e-18;
Matches 42; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 TLVWGFQVDSRGSGCTSDNAAALNASSKEALQIREKIPAAALFQPHNLNSL 61
D 111 LEMGTFTQDGRSAGGCTANDAYAKANAGSKSEALQIREKIPAAALFQPHNLNSL 170
QY 62 RIFDKTPEP 70
D 171 RVFQPPAP 179

RESULT 7
ID VAL1:PHUV STANDARD; PRT; 349 AA.
AC Q05923;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALL PROTEIN.
OR ALI.
OR Pepper huasteco virus (PHV).
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=28349;
RN SEQUENCE FROM N.A.
RX MEDLINE=8405944;
RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA Rivera-Bustamante R.F.:
RA "Complete nucleotide sequence of pepper huasteco virus: analysis and
RA comparison with bipartite geminiviruses.";
J. Gen. Virol. 74:2225-2231(1993).
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or send an email to license@isb-sib.ch).
EMBL: X70418; G4449856.1;
PIR: S31875; S31875.
InterPro: IPR001191; Gemin1_AL1.
Pfam: PF00799; Gemin1_AL1; 1.
PRINTS: PR00227; GEMCOTALL1.

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DR ProDom: PD000736; Gemini_ALI: 1.
KW ATP-binding. 221 228 ATP (BY SIMILARITY).
FT NP_BIND 349 AA: 39722 MW: 53476CD56370F4 CRC64;
SQ SEQUENCE 349 AA: 39722 MW: 53476CD56370F4 CRC64;

Query Match
Best Local Similarity 62.4%; Score 224; DB 1; Length 349;
Matches 43; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRGCGTSDNDAEALNASKEEALQIIREKIPAAALPOFHNLNSL 60
DB 110 TVEMGEQIDGRSGQSDANDYAKANAGSKQALDYIKELAPRDYVLFHFINSLD 170
OY 61 DRIFDKTPEP 70
DB 170 NRIFDTPEP 179

RESULT 8
ID VAL1_TYLCM STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALI PROTEIN (C1 PROTEIN).
OS Tomato yellow leaf curl virus (strain Harmande) (TYLCV).
SC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
SN NCBI_TaxID=10833;
RX SEQUENCE FROM N.A.
RA Frey-Pour A.; Bendahmane M.; Matzeit V.; Accotto G.P.; Crespi S.;
RA "Tomato yellow leaf curl virus from Sardinia is a
RA whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALI PROTEIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL: M10070; AAA46318.1;
CC InterPro: IPR001191; Gemini_ALI.
CC Pfam: PF00799; Gemini_ALI; 1.
CC PRINTS: PR00227; GEMCOATL1.
CC PRODOM: PD000736; Gemini_ALI; 1.
KW ATP-binding. 222 229 ATP (POTENTIAL).
SQ SEQUENCE 353 AA: 40190 MW: 80FA779DF6029A34 CRC64;

Query Match
Best Local Similarity 60.2%; Score 216; DB 1; Length 353;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRGCGTSDNDAEALNASKEEALQIIREKIPAAALPOFHNLNSL 60
DB 110 TVEMGEFQVDSRGCGTSDNDAEALNASKEEALQIIREKIPAAALPOFHNLNSL 169
OY 61 DRIFDKTPEP 70
DB 170 ERIFKVPPEP 179

RESULT 10
ID VAL1_TMOV STANDARD; PRT; 361 AA.
AC Q06557;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALI PROTEIN.
OS Tomato mottle virus (isolate Florida) (TMOV).
SC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
SN NCBI_TaxID=36449;
RX SEQUENCE FROM N.A.
RA Abouzid A.M.; Poliston J.E.; Hebert E.;
RA "The nucleotide sequence of tomato mottle virus, a new geminivirus
RA isolated from tomatoes in Florida.";
RT J. Gen. Virol. 73:3225-3229(1992).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALI PROTEIN FAMILY.

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L14460; AAC32414.1; -
CC DR PIR: J01870; J01870.
CC DR PIR: A36214; A36214.
CC DR PIR: P000736; GEMC0ATALL.1.
CC DR PRINTS: P000227; GEMC0ATALL.1.
CC DR PRINTS: P000228; GEMC0ATCLVL1.
CC DR PRODOM: PD000736; Gemini_AL1.1.
CC KW ATP-Binding. 222 229 ATP (BY SIMILARITY).
CC FT NP-BIND
CC SQ SEQUENCE 361 AA: 40516 MW: 8138665 CEMAC6950 CRC64:

Query Match 50.24; Score 216; DB 1; Length 361;
Best Local Similarity 57.18; Pred. No. 4.3e-17;
Matches 41; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLWGEFQVDSRGSGCSTNDAAEAALNASKEAALQIREKTPAAALQFHHNLSNL 60
Db 110 TIWGEFQVDSRGSGCSTNDAAEAALNASKEAALQIREKTPAAALQFHHNLSNL 169

Oy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 11
ID VAL1.ABMYW STANDARD; PRT: 355 AA.
AC P21947;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALL PROTEIN.
OS AC1 PROTEIN.
CN AC1
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid:10816;
RN [1]
RP SELLINGE-91029584; PubMed-2219703;
RA PIR: A36214; A36214.1.
RA PIR: P000736; GEMC0ATALL.1.
RT "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
RT as well as eukaryotic features".
RL Virology 178:461-468 (1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X15983; -; NOT_ANNOTATED_CDS.
CC DR PIR: A36214; CQCWMI.
CC DR PIR: P000736; GEMC0ATALL.1.
CC DR PRINTS: P000227; GEMC0ATALL.1.
CC DR PRINTS: P000228; GEMC0ATCLVL1.
CC DR PRODOM: PD000736; Gemini_AL1.1.
CC KW ATP-Binding. 221 228 ATP (POTENTIAL).
CC FT NP-BIND
CC SQ SEQUENCE 355 AA: 40237 MW: 16A2CABA63251E95 CRC64:

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Y01444; -; NOT_ANNOTATED_CDS.
CC DR INTERPRO: IPR001191; Gemini_AL1.
CC DR Pfam: PF00759; Gemini_AL1.1.
CC DR PRINTS: P000227; GEMC0ATALL.1.
CC DR PRINTS: P000228; GEMC0ATCLVL1.
CC DR PRODOM: PD000736; Gemini_AL1.1.
CC KW ATP-Binding. 222 228 ATP (POTENTIAL).
CC FT NP-BIND
CC SQ SEQUENCE 358 AA: 40889 MW: 39445FC0B9C333 CRC64:

Query Match 59.1%; Score 212; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 1.2e-16;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLWGEFQVDSRGSGCSTNDAAEAALNASKEAALQIREKTPAAALQFHHNLSNL 60
Db 110 TIWGEFQVDSRGSGCSTNDAAEAALNASKEAALQIREKTPAAALQFHHNLSNL 169

Oy 61 DRIFDKTPEP 70
Db 170 OKIFORPPDP 179

RESULT 13
ID VAL1.TYLCV STANDARD; PRT: 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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Oy 19 OTSNDAAAEALNASSKEEALQIIREKIPAAALQOFHNLNSNLDRIEDKTPE 69
Db 269 KUTKSLSILNVPQEOMLLOPPKLRSPAVALYFYKTAMSNISEVYQETPE 319

Search completed: January 3, 2002, 15:57:16
Job time: 1102 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: January 3, 2002, 15:56:25 : Search time 131.69 Seconds
(without alignments)
77.751 Million cell updates/sec

US-09-289-346a-5
Pairfit score: 359
Sequences: 1 TLVWGEFQDGRSARGCQT.....QFHHNLSNLDRIFDKTPPEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL17.*
1: sp.archae.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mycota.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertibrate.*
14: sp.unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	296	82.5	352	12	Q9E000
2	287	79.9	226	12	Q9WHF6
3	277	77.2	361	12	Q67574
4	275	76.6	225	12	Q9QDB1
5	275	76.6	225	12	Q9QDB1
6	271	75.5	165	12	Q9B653
7	271	75.5	314	12	Q9LIT8
8	271	75.5	364	12	Q9Q555
9	264	73.5	149	12	P88975
10	264	73.5	190	12	Q9Z089
11	264	73.5	190	12	Q9Z084
12	264	73.5	233	12	Q9Z0A4
13	264	73.5	233	12	Q9Z0A4
14	263	73.3	208	12	Q9Z0C4
15	261	72.7	208	12	Q9Z0C0
16	261	72.7	208	12	Q9Z0B8
17	259	72.1	208	12	Q9Z0B6
18	258	71.9	203	12	Q9Z0B3
19	258	71.9	234	12	Q39180

20 251 69.9 208 12 Q9Z0A0
21 251 69.9 363 12 Q9Z0A0
22 251 69.9 363 12 Q9Z0A0
23 251 69.9 363 12 Q9Z0A0
24 251 69.9 363 12 Q9Z0A0
25 249 69.4 349 12 Q88888
26 249 69.4 363 12 Q9Z0A0
27 248 69.1 360 12 Q9Z0A0
28 246 68.5 360 12 Q9Z0A0
29 246 68.5 360 12 Q9Z0A0
30 245 68.2 360 12 Q9Z0A0
31 245 68.2 360 12 Q9Z0A0
32 245 68.2 360 12 Q9Z0A0
33 244 68.0 231 12 Q9Z0A0
34 244 68.0 354 12 Q9Z0A0
35 244 68.0 359 12 Q9Z0A0
36 244 68.0 359 12 Q9Z0A0
37 244 68.0 359 12 Q9Z0A0
38 244 68.0 359 12 Q9Z0A0
39 244 68.0 359 12 Q9Z0A0
40 243 67.7 359 12 Q9Z0A0
41 239 66.6 362 12 Q9Z0A0
42 239 66.6 362 12 Q9Z0A0
43 237 66.0 358 12 Q9Z0A0
44 237 66.0 358 12 Q9Z0A0
45 236 65.7 360 12 Q9Z0A0

ALIGNMENTS

RESULT 1
ID Q9E000 PRELIMINARY: PRT; 352 AA.
AC Q9E000: 2001 (TRENBL) 16, Created)
DT 01-MAR-2001 (TRENBL) 17, Last sequence update)
DE 01-JUN-2001 (TRENBL) 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN.
GN ACL

OS Tomato rugose mosaic virus.
OC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
OK NCBI_Taxid=134599;
PN
RA Sequence from N.A.
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
RA Zambolim E.M., Zerbini F.M.,
RT "Molecular Cloning and Characterization of Tomato rugose mosaic virus
(TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,
RT Minas Gerais, Brazil.";
RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF291960.1; GenBank: AF291960.1; DDBJ: AF291960.1.
DR PFAM: PF00799; Geminin_A1; 1.
DR PRINTS: PR00227; GEMCOATALL.
DR ProDom: PD000736; Geminin_A1; 1.
SO Sequence 352 AA; 40012 MW; 47CD55838E2D613 CRC64;

Query Match 82.5%; Score 296; DB 12; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.1e-26;
Matches 56; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRSARGCQTSDNAEALNASSKEALQITREKIPAAALQFHHNLSNL 60
DB 111 TLVWGEFQDGRSARGCQTSDNAEALNASSKEALQITREKIPAAALQFHHNLSNL 170
QY 61 DRIFDKTPPEP 70
DB 171 DRIFDKTPPEP 180

RESULT 2

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05MHF6
ID 09WHF6 PRELIMINARY; PRT: 226 AA.
AC 09WHF6;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS tomato mild mottle geminivirus.
OC VIRUSES: ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
OX NCBI_TaxID=92943;
RN 1
RC STRAIN=HN96-H5K;
RP SEQUENCE FROM N.A.
RA Maxwell D.P.;
RA Nakhla M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RT "Molecular characterization and DNA-based detection methods for
RT vegetable-infecting geminiviruses in Central America.";
RL Submitted (F85-1999) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR001191; Gemin_Ali.
DR Pfam: PF00759; Gemin_Ali.1
DR PRINTS: PR00227; GEMCOTAL1.
DR ProDom: PD000736; Gemin_Ali. 1.
FT NON_TER 226 226
SQ SEQUENCE 226 AA; 25941 MW; 2BA116712871A23 CRC64;

Query Match 79.9%; Score 287; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 2.7e-25;
Matches 54; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Oy 1 TLVGFQDVSARGGCGQTNDAAEAALNASSKEALQIREKIPAAALFOFINLSSNL 60
Db 111 TIEGFQDVSARGGCGQTNDAAEAALNASSKEAMRIKREKLPKFLFOYINLSSNL 170

Oy 61 DRIFDKTEPP 70
Db 171 DRIFAKAPEP 180

RESULT 3
ID 067574 PRELIMINARY; PRT: 361 AA.
AC 067574;
DT 01-NOV-1996 (T-EMBLrel. 04, Created)
DT 01-NOV-1996 (T-EMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN REP.
OS Golden mosaic virus
OC VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN 1
RC SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RL "Mycopathology 81:980-985(1991).
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RL Plant Dis. 75:336-342(1991).
RN 13
RN SEQUENCE FROM N.A.
RA Gilbertson R.L.;
RA Faria J.C., Ahlquist P.G., Maxwell D.P.;
DR InterPro: IPR001191; Gemin_Ali.
DR Pfam: PF00759; Gemin_Ali.1.
DR PRINTS: PR00227; GEMCOTAL1.
DR ProDom: PD000736; Gemin_Ali. 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 79.9%; Score 287; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 2.7e-25;
Matches 54; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Oy 1 TLVGFQDVSARGGCGQTNDAAEAALNASSKEALQIREKIPAAALFOFINLSSNL 60
Db 111 TIEGFQDVSARGGCGQTNDAAEAALNASSKEAMRIKREKLPKFLFOYINLSSNL 170

Oy 61 DRIFDKTEPP 70
Db 171 DRIFAKAPEP 180

RESULT 3
ID 067574 PRELIMINARY; PRT: 361 AA.
AC 067574;
DT 01-NOV-1996 (T-EMBLrel. 04, Created)
DT 01-NOV-1996 (T-EMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN REP.
OS Golden mosaic virus
OC VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10839;
RN 1
RC SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RL "Mycopathology 81:980-985(1991).
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RL Plant Dis. 75:336-342(1991).
RN 13
RN SEQUENCE FROM N.A.
RA Gilbertson R.L.;
RA Faria J.C., Ahlquist P.G., Maxwell D.P.;
DR InterPro: IPR001191; Gemin_Ali.
DR Pfam: PF00759; Gemin_Ali.1.
DR PRINTS: PR00227; GEMCOTAL1.
DR ProDom: PD000736; Gemin_Ali. 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 77.2%; Score 277; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 6.5e-24;
Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 4 WGEFQDVSARGGCGQTNDAAEAALNASSKEALQIREKIPAAALFOFINLSSNL 63
Db 113 WGEFQDVSARGGCGQTNDAAEAALNASSKEAMQIKREKLPKFLFOYINLSSNL 172

Oy 64 FKDTPEP 70
Db 173 FKAPDP 179

RESULT 4
ID 09QDB1 PRELIMINARY; PRT: 225 AA.
AC 09QDB1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS cowpea golden mosaic geminivirus.
OC VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=69263;
RN 1
RC STRAIN=CGM4-BR;
RP SEQUENCE FROM N.A.
RA Faria J.C.;
RA "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RA Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR001191; Gemin_Ali.
DR Pfam: PF00759; Gemin_Ali.1.
DR PRINTS: PR00227; GEMCOTAL1.
DR ProDom: PD000736; Gemin_Ali. 1.
FT NON_TER 225 225
SQ SEQUENCE 225 AA; 10895CB6BD8D15B5D CRC64;

Query Match 76.5%; Score 275; DB 12; Length 225;
Best Local Similarity 76.8%; Pred. No. 6.6e-24;
Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Oy 4 WGEFQDVSARGGCGQTNDAAEAALNASSKEALQIREKIPAAALFOFINLSSNL 63
Db 113 WGEFQDVSARGGCGQTNDAAEAALNASSKEAMQIKREKLPKFLFOYINLSSNL 172

Oy 64 FKDTPEP 70
Db 173 FKAPDP 179

RESULT 5
ID 009727 PRELIMINARY; PRT: 225 AA.
AC 009727;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN REP.
OS Leonurus mosaic virus.
OC VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=59177;
RN 1
RC STRAIN=LEMV-BRAZIL;
RP SEQUENCE FROM N.A.
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

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ID P88975; PRELIMINARY; PRT; 149 AA.
AC
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN AC1.
OS Macrotellium golden mosaic geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN (1) SEQUENCE FROM N.A.
RC STRAIN-JAMAICA;
RA ROYE M.E.;
RL EMBL: U75278; AAB3619.1;
RL InterPro: IPR001191; Gemin_ALI.
DR Pfam: PF00799; Gemin_ALI; 1.
DR PRINTS: PR00227; GEMCATAL1.
DR PRODOM: PD000736; Gemin_ALI; 1.
DR NON_TER 149
FT NON_TER 149
SQ SEQUENCE 149 AA; 15785 MW; E4CF5ED4C9CD508 CRC64;

Query Match 73.5%; Score 264; DB 12; Length 149;
Best Local Similarity 62.4%; Pred. No. 7.5e-23;
Matches 49; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGEFQIDGRSARGCGCOTNDAAAEALNASKEEAALQIIREKIPAAALFOFHNSNL 60
DB 52 TLWGEFQIDGRSARGCGCOTNDAAAEALNASKEEAALQIIREKIPAAALFOFHNSNL 111
OY 61 DRIFDKTPPEP 70
DB 112 DRIFDKDPEP 121

RESULT 10
OY2089
ID O92089; PRELIMINARY; PRT; 190 AA.
AC
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE C1 AND C4 GENES, CLONE YOKOHAMA3-1, PARTIAL AND COMPLETE CDS (FRAGMENT).
DE C1.
OS tobacco leaf curl virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN (1) SEQUENCE FROM N.A.
RC STRAIN-YOKOHAMA3;
RA OOI K., Ohshita S., Ishii I., Yahara T.;
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001315; BAA34033.1;
DR InterPro: IPR001191; Gemin_ALI.
DR Pfam: PF00799; Gemin_ALI; 1.
DR PRINTS: PR00227; GEMCATAL1.
DR PRODOM: PD000736; Gemin_ALI; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 190 AA; 21432 MW; AAC093D1D1610FAD CRC64;

Query Match 73.5%; Score 264; DB 12; Length 190;
Best Local Similarity 62.4%; Pred. No. 9.9e-23;
Matches 53; Conservative 6; Mismatches 10; Indels 16; Gaps 1;

OY 1 TLWGEFQIDGRSARGCGCOTNDAAAEALNASKEEAALQIIREKIPAAALFOFHNSNL 60
DB 85 TLWGEFQIDGRSARGCGCOTNDAAAEALNASKEEAALQIIREKIPAAALFOFHNSNL 144
OY 61 DRIFDKTPPEP 69
DB 145 DRIFAPLEVPCVFASSEDOVPE 169

RESULT 12
OY2089
ID OY2089; PRELIMINARY; PRT; 233 AA.
AC
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
DE REP.
OS Macrotellium golden mosaic geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN (1) SEQUENCE FROM N.A.
RC STRAIN-JAMAICA STRAIN 1;
RA ROYE M.E.;
RL Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica. Plant Dis. 82:121-123 (1998).
DE Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
RN 121
RC SEQUENCE FROM N.A.
RA ROYE M.E., McLaughlin W.A., Maxwell D.P.;
RL "Molecular characterization of two distinct geminiviruses infecting M.

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DB 85 TLENGTFQIDGRSARGCGCOTNDAAAEALNASKEEAALQIIREKIPAAALFOFHNSNL 144
OY 61 DRI-----FDRKTPPE 69
DB 145 DRIFAPLEVPCVFASSEDOVPE 169

RESULT 11
OY2084
ID O92084; PRELIMINARY; PRT; 190 AA.
AC
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE C1 AND C4 GENES, CLONE YOKOHAMA5-2, PARTIAL AND COMPLETE CDS (FRAGMENT).
DE C1.
OS tobacco leaf curl virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN (1) SEQUENCE FROM N.A.
RC STRAIN-YOKOHAMA5;
RA OOI K., Ohshita S., Ishii I., Yahara T.;
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001318; BAA34039.1;
DR InterPro: IPR001191; Gemin_ALI.
DR Pfam: PF00799; Gemin_ALI; 1.
DR PRINTS: PR00227; GEMCATAL1.
DR PRODOM: PD000736; Gemin_ALI; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 190 AA; 21444 MW; AACIC2943E3F01AD CRC64;

Query Match 73.5%; Score 264; DB 12; Length 190;
Best Local Similarity 62.4%; Pred. No. 9.9e-23;
Matches 53; Conservative 6; Mismatches 10; Indels 16; Gaps 1;

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DB 85 TLENGTFQIDGRSARGCGCOTNDAAAEALNASKEEAALQIIREKIPAAALFOFHNSNL 144
OY 61 DRI-----FDRKTPPE 69
DB 145 DRIFAPLEVPCVFASSEDOVPE 169

RESULT 12
OY2089
ID OY2089; PRELIMINARY; PRT; 233 AA.
AC
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
DE REP.
OS Macrotellium golden mosaic geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51676;
RN (1) SEQUENCE FROM N.A.
RC STRAIN-JAMAICA STRAIN 1;
RA ROYE M.E.;
RL Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica. Plant Dis. 82:121-123 (1998).
DE Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
RN 121
RC SEQUENCE FROM N.A.
RA ROYE M.E., McLaughlin W.A., Maxwell D.P.;
RL "Molecular characterization of two distinct geminiviruses infecting M.

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lathyrus from Jamaica.";
RT Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF098940; AADI7850.1; -.
DR InterPro: IPR001191; Gemini_All.
DR Pfam: PF00799; Gemini_Al_1.
DR PRMS: PK00229; GEMCOTALL.
DR PTM: PD00626; Gemini_Al_1.
FT NON_TER 233 AA.
SQ SEQUENCE 233 AA: 2635 MW: AA49QAF4D2I6GA02 CRC64;

Query Match              73.5%   Score 264; DB 12; Length 233;
Best Local Similarity    70.0%; Pred. No. 1, 2e-22;
Matches 49; Conservative 1; Mismatches 10; Indels 0; Gaps
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Db       110 TIEWGVOFDGRSARGCGQTSDNAAEALNSGTGAAMRVKELPKFLFYOHNLSSL 169

OY      61 DRIFDKTPEP 70
Db       170 DRIFDKAPEP 179

RESULT 13
ID Q9W827 PRELIMINARY: PRT; 190 AA.
AC O9W827; 1999 (TRIMBLER 12, Created)
DT 01-NOV-1999 (TRIMBLER 11, Last annotation update)
DE C1 PROTEIN (FRAGMENT).
DI 01-JUN-2001 (TRIMBLER 17, Last annotation update)
DS C1
GN GN tobacco leaf curl virus.
CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=67762;
OC VIRUS
NC NCBIs: REFSEQ
RC STRAIN=GORA3.
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001303; BAA34010.1; -.
DR InterPro: IPRO01191; Gemini_All.
DR PRMS: PK00229; GEMCOTALL.
DR PTM: PD00736; Gemini_Al_1.
DR Problem: PD00736; Gemini_Al_1.
FT NON_TER 1 190
FT NON_TER 190 AA.
SQ SEQUENCE 190 AA: 21444 MW: 93C374ZA8EBDBYTE CRC64;

Query Match              73.3%   Score 263; DB 12; Length 190;
Best Local Similarity    62.4%; Pred. No. 1, 3e-22;
Matches 53; Conservative 6; Mismatches 10; Indels 16; Gaps
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          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       85 TLWGTFQVDGRSGRGCGQNADCAFAALNAASKAALSITREKLPKDFIOYHNLNSL 144

OY      61 DRI-----FKATPE 69
Db       145 DRIFAPPLFFVFCFSSFSQQVE 169

RESULT 14
ID Q9Z0C4 PRELIMINARY: PRT; 208 AA.
AC Q9Z0C4; 1999 (TRIMBLER 10, Created)
DT 01-MAY-1999 (TRIMBLER 10, Last annotation update)
DE C1 AND C4 GENES. CLONE ABUR43-1. PARTIAL AND COMPLETE CDS (FRAGMENT).
DI 01-JUN-2001 (TRIMBLER 17, Last annotation update)
DS C1 AND C4
GN C1 AND C4
CC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxId=67762;
OC VIRUS
NC NCBIs: REFSEQ
RC STRAIN=ABUR43-1.
RA Ooi K., Ohshita S., Ishii I., Yahara T.;
RT "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
RL J. Plant Res. 110:247-257(1997).
DR EMBL: AB001303; BAA34010.1; -.
DR InterPro: IPRO01191; Gemini_All.
DR PRMS: PK00229; GEMCOTALL.
DR PTM: PD00736; Gemini_Al_1.
DR Problem: PD00736; Gemini_Al_1.
FT NON_TER 1 190
FT NON_TER 190 AA.
SQ SEQUENCE 190 AA: 21444 MW: 93C374ZA8EBDBYTE CRC64;
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Search completed: January 3, 2002, 15:56:25
Job time: 1121 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:49 ; Search time 65.28 seconds
(without alignments)
24,130 Million cell updates/sec

Title: US-09-289-346a-5

Perfit score: 359

Sequence: 1 TLVWGEFQVDCRSARGCQT.....EUFHNLNSLRIDFKTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/ACTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/Bactillesi.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	220	61.3	361	4 US-08-838-151A-2
2	220	61.3	361	4 US-08-838-151A-4
3	220	61.3	361	4 US-08-838-151A-6
4	219	61.0	359	4 US-08-809-103B-2
5	219	61.0	359	4 US-08-809-103B-4
6	219	61.0	359	4 US-08-809-103B-6
7	219	61.0	359	4 US-08-809-103B-8
8	219	61.0	359	4 US-08-809-103B-8
9	218	60.7	353	4 US-08-838-151A-44
10	218	60.7	353	4 US-08-838-151A-46
11	218	60.7	353	4 US-08-838-151A-49
12	218	60.7	353	4 US-08-838-151A-52
13	218	60.7	353	4 US-08-838-151A-52
14	203	55.5	337	4 US-08-838-151A-24
15	203	55.5	337	4 US-08-838-151A-27
16	203	55.5	337	4 US-08-838-151A-30
17	195	54.3	357	4 US-08-838-151A-20
18	63.5	17.7	1713	3 US-08-600-982-24
19	63.5	17.7	1713	5 PCT-US94-10261A-24
20	59.5	16.6	2161	1 US-07-246-204B-2
21	59.5	16.6	2161	1 US-08-455-543A-49
22	59.5	16.6	2161	1 US-08-455-543A-51
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24	59.5	16.6	2161	2 US-08-223-305C-49
25	59.5	16.6	2161	2 US-08-311-363-51
26	59.5	16.6	2161	2 US-08-311-363-51
27	58.5	16.3	374	2 US-08-928-692-51

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29 56 15.6 171 4 US-08-170-956-22
30 56 15.6 416 4 US-09-416-050A-4
31 56 15.6 416 4 US-09-416-800-4
32 56 15.6 416 4 US-09-569-569-4
33 56 15.6 416 4 US-09-569-569-4
34 54.5 15.2 3898 2 US-08-876-991-2
35 54.5 15.2 3898 2 US-05-059-453-2
36 54 15.0 242 2 US-08-624-352A-3
37 54 15.0 242 3 US-08-826-390-3
38 54 15.0 271 1 US-08-876-919-10
39 54 15.0 271 1 US-08-776-088-13
40 54 15.0 271 1 US-08-776-088-13
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42 54 15.0 274 5 PCT-US95-09145A-15
43 54 15.0 325 1 US-08-276-919-4
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ALIGNMENTS

RESULT 1
US-08-838-151A-2
: Sequence 2, Application US/08B38151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Luu, Haog T
: APPLICANT: Luu, Haog T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: INVENTOR: Hanson, Steve
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: FILING AGENT:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SV33801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5400
: INFORMATION FOR SEQ ID NO. 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 61.3% Score 220; DB 4; Length 361;
Best Local Similarity 58.6%; Pred. No. 2.3e+21;
Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TLVWGEFQVDCRSARGCQTSSARAAALNASKEALQILREKIPAAALPOFHNLNSL 60

Db 110 TIWGEQVQDSRGAGCQTSNDAAEAALNASKEEPAALQIREKIPAAALQFPHNINSL 169
Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 2
US-08-838-151A-4
: Sequence 4, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-4

Query Match 61.3%, Score 220; DB 4; Length 361;
Best Local Similarity 58.6%; Pred. No. 2.3e-21;
Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
Qy 1 TLWGEQVQDSRGAGCQTSNDAAEAALNASKEEPAALQIREKIPAAALQFPHNINSL 60
Db 110 TIWGEQVQDSRGAGCQTSNDAAEAALNASKEEPAALQIREKIPAAALQFPHNINSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 3
US-08-838-151A-6
: Sequence 6, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T

: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 361 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-838-151A-6

Query Match 61.3%, Score 220; DB 4; Length 361;
Best Local Similarity 58.6%; Pred. No. 2.3e-21;
Matches 41; Conservative 14; Mismatches 15; Indels 0; Gaps 0;
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Db 110 TIWGEQVQDSRGAGCQTSNDAAEAALNASKEEPAALQIREKIPAAALQFPHNINSL 169

Qy 61 DRIFDKTPEP 70
Db 170 ERIFAKAPEP 179

RESULT 4
US-08-838-151A-8
: Sequence 8, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 05/08/93B,151A
 FILING DATE: 05/08/93B,151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-B

Query Match 61.3% Score 220; DB 4; Length 361;
 Best Local Similarity 58.6%; Fred. No. 2.3e-21;
 Matches 41; Conservative 14; Mismatches 15; Indels 0;

QY 1 TLVMEQFQVDSARGCGQTSNDAAEALNASSKEALQITREKIPAAALFQPHRLNSNL 60
 DB 111 TLVMEQFQVDSARGCGQTSNDAAEALNASSKEALQITREKIPAAALFQPHRLNSNL 60
 QY 61 DRIFDKTEP 70
 DB 170 ERIFAKAPEP 179

RESULT 5
 US-08-809-103B-2
 Sequence 2, Application US/08809103B
 Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GRONENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 05/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94.11040
 FILING DATE: 15-SEP-1994
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 TELEPHONE: (703) 521-2237

TELEFAX: (703) 685-0573
 TELEX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-2

Query Match 61.0% Score 219; DB 4; Length 359;
 Best Local Similarity 58.0%; Fred. No. 3.1e-21;
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 2 LVMEQFQVDSARGCGQTSNDAAEALNASSKEALQITREKIPAAALFQPHRLNSNL 61
 DB 111 LVMEQFQVDSARGCGQTSNDAAEALNASSKEALQITREKIPAAALFQPHRLNSNL 61
 QY 62 DRIFDKTEP 70
 DB 171 KVFQVPPAP 179

RESULT 6
 US-08-809-103B-4
 Sequence 4, Application US/08809103B
 Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GRONENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 05/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA: FR 94.11040
 APPLICATION NUMBER: 15-SEP-1994
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-4

Query Match 61.0% Score 219; DB 4; Length 359;

Best Local Similarity 58.0%; Pred. No. 3.1e-21:
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
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 Db 111 LKMGTFQIDGSRSGQGTANDAYAKAINAGSKSQALDVIKELAPROYVLHFHNINSLD 170
 Oy 62 RIFDKTPEP 70
 Db 171 KVFQVPPAP 179

RESULT 7
 US-08-809-103B-6
 : Sequence 6, Application US/08809103B
 : Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GROENBORN, BRUNO
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : NUMBER OF SEQUENCES: 17
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: YOUNG & THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA: US/08/809,103B
 : FILING DATE: 17-MAR-1997
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: FR 94.11040
 : FILING DATE: 15-SEP-1994
 : PCT APPLICATION DATA:
 : APPLICATION NUMBER: NO PCT/FR95/01192
 : FILING DATE: 15-SEP-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PATCH, Andrew J.
 : REGISTRATION NUMBER: 32,925
 : REFERENCE/DOCKET NUMBER: US94AL CNR TOM
 : TELEPHONE: (703) 521-2297
 : TELEFAX: (703) 685-0573
 : TELEX: 248425 EMBON
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 359 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-809-103B-6

Query Match 61.0%; Score 219; DB 4; Length 359;
 Best Local Similarity 58.0%; Pred. No. 3.1e-21;
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
 Oy 2 LVKGEFQVDSRGSGQTSNDAAALNASSKEALQIREKIPAAALFQFHNLNSLD 61
 Db 111 LKMGTFQIDGSRSGQGTANDAYAKAINAGSKSQALDVIKELAPROYVLHFHNINSLD 170
 Oy 62 RIFDKTPEP 70
 Db 171 KVFQVPPAP 179

RESULT 8
 US-08-809-103B-8
 : Sequence 8, Application US/08809103B
 : Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GROENBORN, BRUNO
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : NUMBER OF SEQUENCES: 17
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: YOUNG & THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA: US/08/809,103B
 : FILING DATE: 17-MAR-1997
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: FR 94.11040
 : FILING DATE: 15-SEP-1994
 : PCT APPLICATION DATA:
 : APPLICATION NUMBER: NO PCT/FR95/01192
 : FILING DATE: 15-SEP-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PATCH, Andrew J.
 : REGISTRATION NUMBER: 32,925
 : REFERENCE/DOCKET NUMBER: US94AL CNR TOM
 : TELEPHONE: (703) 521-2297
 : TELEFAX: (703) 685-0573
 : TELEX: 248425 EMBON
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 359 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-809-103B-8

Query Match 61.0%; Score 219; DB 4; Length 359;
 Best Local Similarity 58.0%; Pred. No. 3.1e-21;
 Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
 Oy 2 LVKGEFQVDSRGSGQTSNDAAALNASSKEALQIREKIPAAALFQFHNLNSLD 61
 Db 111 LKMGTFQIDGSRSGQGTANDAYAKAINAGSKSQALDVIKELAPROYVLHFHNINSLD 170
 Oy 62 RIFDKTPEP 70
 Db 171 KVFQVPPAP 179

RESULT 9
 US-08-838-151A-44
 : Sequence 44, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: SLOUT, John T
 : APPLICANT: Luu, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
 : MOLECULE TYPE: Genes

```

;
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

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```

Query Match      60.7% Score 218 DB 4; Length 353;
Best Local Similarity 60.0%; Pred. No. 4.1e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

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OY 1 TLVWGFEQVDSRGSGCOTNDAAAEALNASKEEALQITREKIPAAALQFHHNLSNL 60
DB 110 TLVWGFEQVDSRGSGCOTNDAAAEALNASKEEALQITREKIPAAALQFHHNLSNL 60
OY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

```

```

RESULT 10
; US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; APPLICANT: Stu. John T
; APPLICANT: Luu, Haog T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; ADDRESS/SEQUENCE NUMBER: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

```

```

;
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

```

```

Query Match      60.7% Score 218 DB 4; Length 353;
Best Local Similarity 60.0%; Pred. No. 4.1e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

```

```

OY 1 TLVWGFEQVDSRGSGCOTNDAAAEALNASKEEALQITREKIPAAALQFHHNLSNL 60
DB 110 TLVWGFEQVDSRGSGCOTNDAAAEALNASKEEALQITREKIPAAALQFHHNLSNL 60
OY 61 DRIFDKTPEP 70
DB 170 ERIFVKVPEP 179

```

```

RESULT 11
; US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; APPLICANT: Stu. John T
; APPLICANT: Luu, Haog T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; ADDRESS/SEQUENCE NUMBER: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rockey, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```


ADDRESS: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-838-151A-24

Query Match 56.5%: Score 203; DB 4; Length 357;
 Best Local Similarity 65.6%: Pred. No. 4.2e-19;
 Matches 40; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
 Oy 4 WGEFVDGSRAGCGOOTSNDAAAEALNASSKTEALQITREKIPAAALFQPHNLNSLDRI 63
 Db 111 FGVQIDGRSARGQOQANDAYAEALNNGSKSEALNILKEKPKDYTLQFHNLSNLDRI 170
 Oy 64 F 64
 Db 171 F 171

RESULT 15
 US-08-838-151A-27
 Sequence 27, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Rocky, John T
 APPLICANT: John, Haug T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE:
 ADDRESS: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-838-151A-27
 Query Match 56.5%: Score 203; DB 4; Length 357;
 Best Local Similarity 65.6%: Pred. No. 4.2e-19;
 Matches 40; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
 Oy 4 WGEFVDGSRAGCGOOTSNDAAAEALNASSKTEALQITREKIPAAALFQPHNLNSLDRI 63
 Db 111 FGVQIDGRSARGQOQANDAYAEALNNGSKSEALNILKEKPKDYTLQFHNLSNLDRI 170
 Oy 64 F 64
 Db 171 F 171
 Search completed: January 3, 2002, 15:38:50
 Job time: 227 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:37 ; Search time 144.17 Seconds
(without alignments)
35.965 Million cell updates/sec

Title: US-09-289-346a-6
Perfect score: 357
Sequence: 1 TLVAGFQVDRSGRCQT.....EFAALNSLDRFDXTP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT.*
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22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357	100.0	70	21	AA18682
2	340	95.2	70	21	AA18677
3	340	95.2	356	21	AA18687
4	332	93.0	70	21	AA18685
5	328	91.3	70	21	AA18682
6	326	91.3	70	21	AA18689
7	326	91.3	70	21	AA18684
8	326	91.3	70	21	AA18690
9	325	91.0	70	21	AA18678
10	325	91.0	70	21	AA18676
11	324	90.9	70	21	AA18689

12	322	90.2	70	21	AA18680	Mutant peptide der
13	322	90.2	70	21	AA18691	Mutant peptide der
14	319	89.4	70	21	AA18681	Mutant peptide der
15	318	89.1	70	21	AA18683	Mutant peptide der
16	308	86.3	70	21	AA18679	Mutant peptide der
17	210	58.8	359	17	AA188870	Sardinian tomato y
18	210	58.8	359	17	AA188871	Sardinian tomato y
19	210	58.8	359	17	AA188872	Sardinian tomato y
20	206	57.7	353	18	AAW34338	Bean golden mosaic
21	206	57.7	353	18	AAW34332	Bean golden mosaic
22	206	57.7	353	18	AAW34333	Bean golden mosaic
23	206	57.7	353	18	AAW34334	Bean golden mosaic
24	206	57.7	353	18	AAW34335	Bean golden mosaic
25	204	57.1	353	8	AA170407	ORF 4, gene product
26	204	57.1	361	18	AAW34336	Tomato mottle viru
27	204	57.1	361	18	AAW34324	Tomato mottle viru
28	204	57.1	361	18	AAW34325	Tomato mottle viru
29	204	57.1	361	18	AAW34326	Tomato mottle viru
30	195	53.8	353	8	AA170408	Product of ORF 4
31	195	53.8	353	8	AA170409	Product of ORF 4
32	191	53.5	357	18	AAW34329	Tomato yellow leaf
33	191	53.5	357	18	AAW34330	Tomato yellow leaf
34	191	53.5	357	18	AAW34331	Tomato yellow leaf
35	183	51.3	357	18	AAW34337	Tomato yellow leaf
36	67	18.8	447	21	AA199659	Human GPase assoc
37	67	18.8	447	21	AA199659	Human GPase assoc
38	67	18.8	447	21	AA199659	Human GPase assoc
39	67	18.8	447	21	AA199659	Human GPase assoc
40	67	18.8	447	21	AA199659	Human GPase assoc
41	67	18.8	447	21	AA199659	Human GPase assoc
42	67	18.8	456	21	AA187190	Human secreted pro
43	67	18.8	456	21	AA187190	Human secreted pro
44	64.5	18.1	1693	21	AA18457	Human gene 26 enco
45	64.5	18.1	1693	21	AA18457	Human gene 26 enco

ALIGNMENTS

RESULT	1
AA18682	ID
AA18682	AA18682 standard; peptide; 70 AA.
AA18682	AA18682;
22	JAN-2001 (first entry)
XX	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
DE	Geminivirus: replication protein; Rep protein; AL1: transgenic plant;
XX	ribosome binding region; resistance: geminivirus infection.
KW	Synthetic.
XX	Tomato golden mosaic virus.
OS	Tomato golden mosaic virus.
XX	Key
XX	Location/Qualifiers
FT	Misc-difference 52
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 54
FT	/note= "wild type residue replaced with Ala"
FT	Misc-difference 51
FT	/note= "wild type residue replaced with Ala"
XX	WO200054573-A1.
PN	21-SEP-2000.
XX	15-MAR-2000. 2000WO-US06759.
PD	18-MAR-1999; 99US-0125004.
XX	09-APR-1999; 99US-0289346.
PR	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	

XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI: 2000-618851/59.
 XX
 DR Transgenic plants with increased resistance to geminivirus infection
 XX containing a nucleic acid sequence
 XX encoding a mutant A11 protein with a mutation in the 8b binding region
 PT
 XX
 SS Claim 53: Page 44-45; 73pp: English.
 CC
 CC The present sequence represents a mutant peptide, derived from a
 CC double-stranded DNA, which is also known as A11. A11 binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the A11 protein are used
 CC to produce transgenic plants. The mutation in A11 is present in a
 CC ribosome binding region, and expression of mutant A11 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant A11
 CC protein is useful for producing plants having increased resistance to a
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ

Query Match 100.0%; Score 357; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 6.2e-38;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TLVWGFQVDRSARGCOTSDNAAAEALNASKEEALQIIRKIPKYLFAFALNSNL 60
 Db 1 TLVWGFQVDRSARGCOTSDNAAAEALNASKEEALQIIRKIPKYLFAFALNSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 61 drifdktp 70

RESULT 2
 ID AAB18677 standard; peptide; 70 AA.
 XX
 AC AAB18677;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Peptide fragment from Rep protein of TGMV (amino acids 110-179).
 XX
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 OS Tomato golden mosaic virus.
 XX
 PN WO2000054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06755.
 XX
 PR 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 XX
 PA (UNIC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 DR WPI: 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection

PT Transgenic plants with increased resistance to geminivirus infection
 XX comprising a nucleic acid construct containing a nucleic acid sequence
 XX encoding a mutant A11 protein with a mutation in the 8b binding region
 PT
 XX
 SS Disclosure; Page 18; 73pp: English.
 CC
 CC The present sequence is derived from a geminivirus replication (Rep)
 CC protein, which is also known as A11. A11 binds double-stranded DNA,
 CC catalyses cleavage and ligation of single-stranded DNA, and interacts
 CC with other viral and host proteins. Mutants of the A11 protein are used
 CC to produce transgenic plants. The mutation in A11 is present in a
 CC ribosome binding region, and expression of mutant A11 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant A11
 CC protein is useful for producing plants having increased resistance to a
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
 CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.
 XX Sequence 70 AA:
 SQ

Query Match 95.2%; Score 340; DB 21; Length 70;
 Best Local Similarity 95.7%; Pred. No. 8.9e-36;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TLVWGFQVDRSARGCOTSDNAAAEALNASKEEALQIIRKIPKYLFAFALNSNL 60
 Db 1 TLVWGFQVDRSARGCOTSDNAAAEALNASKEEALQIIRKIPKYLFAFALNSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 61 drifdktp 70

RESULT 3
 ID AAB18687 standard; peptide; 356 AA.
 XX
 AC AAB18687;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a geminivirus replication protein of TGMV.
 XX
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 OS Tomato golden mosaic virus.
 XX
 PN Key Location/Qualifiers
 XX Misc-difference 354 /note- "unspecified amino acid"
 XX
 XX WO2000054573-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06755.
 XX
 PR 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 XX
 PA (UNIC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 DR WPI: 2000-618851/59.
 XX
 XX Transgenic plants with increased resistance to geminivirus infection

PT	comprise a nucleic acid construct containing a nucleic acid sequence
PP	encoding a mutant A1 protein with a mutation in the Rb binding region
XX	
XX	Claim 53; Page 46; 73pp: English.
CC	The present sequence represents a mutant peptide, derived from a
CC	geminivirus replication (Rep) protein, also known as A1. A1 binds
CC	double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC	DNA, and, with the protein product of the A2 gene, the A1 protein
CC	protein are used to produce transgenic plants. The mutation in A1 is
CC	present in a ribosome binding region, and expression of mutant A1
CC	protein imparts increased resistance to geminivirus infection in the
CC	plant. Mutant A1 proteins are useful for producing plants having an
CC	increased resistance or reduced sensitivity to geminiviruses such as
CC	tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf
CC	curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC	virus, cotton leaf curl virus or beet curly top virus.
XX	Sequence 70: AA:
XX	

Query Match	93.0%	Score 332;	DB 21;	Length 70;	
Best Local Similarity	94.3%	Pos'd No. 9	3e-35;		
Matches 66;	Conservative	0;	Mismatches 4;	Indels 0;	Gaps
QY	1	TLWKEGFQVIGRSARGGCGTSDNDAAGALNASKPEKAQITFEKTPRYLFAFAALNSNI	60		
DB	1	tlwkegfqvgvrsrggqctsdndaaalinasakeaalqfirkelpkyllqfthlnsl	60		
QY	61	DRIFQKTPPEP	70		
DB	61	drifkfktppep	70		
RESULT	5				
AA181688					
ID	AA181688	standard: peptide;	70	AA.	
XX	XX				
XX	AA181688;				
XX	XX				
DT	22-JAN-2001	(first entry)			
DE	Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.				
DE	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;				
KW	ribosome binding region; resistance; geminivirus infection.				
KW	Synthetic;				
OS	Tomato golden mosaic virus.				
XX	XX				
XX	Key	Location/Qualifiers			
FT	Misc-difference 19	/note= "wild type residue replaced with Ala"			
FT	Misc-difference 20	/note= "wild type residue replaced with Ala"			
FT	Misc-difference 20	/note= "wild type residue replaced with Ala"			
PN	WG2000054573-Al.				
XX	XX				
PP	21-SEP-2000.				
XX	XX				
PF	15-MAR-2000;	2000MO-US06759.			
XX	XX				
PR	18-MAR-1999;	99US-0125004.			
PR	09-APR-1999;	99US-0289346.			
PA	(UYNC-) UNIV NORTH CAROLINA STATE.				
XX	XX				
XX	Hanley-Bowdoin L. Orozco BM,	Kong L;			
DR	WPI: 2000-61A851/59.				

PT	comprise a nucleic acid construct containing a nucleic acid sequence		
PT	encoding a mutant A11 protein with a mutation in the Rb binding region		
PT	-		
XX	Claim 53; Page 46; 73pp: English.		
XX	The present sequence represents a mutant peptide derived from a		
XX	geminivirus replicon (Rep) protein, also known as A11. A11 binds		
CC	double-stranded DNA, catalyzes cleavage and ligation of single-stranded		
CC	DNA, and interacts with other viral and host proteins. Mutants of the		
CC	protein are used to produce transgenic plants. The mutation in A11 is		
CC	present in a ribosome binding region, and expression of mutant A11		
CC	protein imparts increased resistance to geminivirus infection in the		
CC	plant. Mutant A11 proteins are useful for producing plants having		
CC	resistance to geminivirus infection, such as tomato yellow leaf		
CC	tomato golden mosaic virus, tomato curly virus, African cassava mosaic		
CC	virus, tomato leaf curl virus, yellow cassava mosaic virus, Indian		
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic		
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper		
CC	virus, cotton leaf curl virus or beet curly top virus.		
XX			
XX	Sequence 70 AA:		
XX			
XX	Query Match 93.0%; Score 332; DB 21: Length 70;		
XX	Best Local Similarity 94.3%; Pred. No. 9.3e-35;		
XX	Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps		
OY	1 TLWGEFQVDRGSRGCGTSSNDAAEALNASSKEFALQITREKIPKYLFAFAAALNSL 60		
DB	1		
OY	1 TLWGEITWYGRSGRGGTSSNDAAEALNASSKEEALIREKIPKYLQIFGMINSL 60		
OY	61 DRFPKTPPEP 70		
OY			
DB	61 DRIFDKTPEP 70		
DB			
RESULT 5			
XX	A118688		
XX	11 A118688 standard; peptide; 70 AA.		
XX	AA118688;		
XX	22-JAN-2001 (first entry)		
DT	Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.		
DE	Geminivirus: replication protein; Rep protein; A11; transgenic plant;		
DE	ribosome binding region; resistance; geminivirus infection.		
KW	Synthetic.		
OS	Tomato golden mosaic virus.		
XX			
XX	Key Location/Qualifiers		
FT	Misc-difference /note= "wild type residue replaced with Ala"		
FT	Misc-difference 20 /note= "wild type residue replaced with Ala"		
XX			
XX	MO2000054573-A1.		
XX			
XX	21-SEP-2000.		
XX			
PF	15-MAR-2000; 2000MC-US06759.		
XX			
PR	18-MAR-1999; 99US-0125004.		
PR	09-APR-1999; 99US-0289346.		
XX			
PA	(UNYC-) UNIV NORTH CAROLINA STATE.		
XX			
XX	Hanley-Bowdoin L. Orozco BM, Kong L;		
DR	WPI: 2000-614851/59.		

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant ALI protein with a mutation in the Rb binding region
 PT
 PS
 XX Disclosure: Page 48; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
 CC protein have been identified that confer increased resistance to ALI
 CC present in a ribosome binding region, and expression of mutant ALI
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant ALI proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;

Query Match 92.2%; Score 329; DB 21; Length 70;
 Best Local Similarity 92.9%; Pct. Id. 3e-34; Mismatches 5; Gaps 0;
 Matches 65; Conservative 0;

OY 1 TLVWGFQVDRSARGCQTSNDAAAEALNAGSKEALQITREKIPKYLFAFAALNSL 60
 DB 1 tlwgfqvdgrsargcqtndaaaealnagskealqirekipekylfqfhnsl 60
 QY 61 DRIFKTPFP 70
 DB 61 drifktpfp 70

RESULT 6
 AAB18692
 ID AAB18692 standard; peptide; 70 AA.
 AC AAB18692;
 AC AAB18692;
 DT 22-JAN-2001 (first entry)
 XX

XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
 XX Geminivirus: replication protein; Rep protein; ALI; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FH Misc-difference 66 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"
 FT Misc-difference 65 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000NO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 XX encoding a mutant ALI protein with a mutation in the Rb binding region
 XX
 PT
 PT
 XX Disclosure: Page 50; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as ALI. ALI binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the ALI
 CC protein are used to produce transgenic plants. The mutation in ALI is
 CC present in a ribosome binding region, and expression of mutant ALI
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant ALI proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;

Query Match 91.9%; Score 328; DB 21; Length 70;
 Best Local Similarity 92.9%; Pct. Id. 3e-34; Mismatches 5; Gaps 0;
 Matches 65; Conservative 0;

OY 1 TLVWGFQVDRSARGCQTSNDAAAEALNAGSKEALQITREKIPKYLFAFAALNSL 60
 DB 1 tlwgfqvdgrsargcqtndaaaealnagskealqirekipekylfqfhnsl 60
 QY 61 DRIFKTPFP 70
 DB 61 drifktpfp 70

RESULT 7
 AAB18684
 ID AAB18684 standard; peptide; 70 AA.
 AC AAB18684;
 AC AAB18684;
 DT 22-JAN-2001 (first entry)
 XX

XX Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.
 XX Geminivirus: replication protein; Rep protein; ALI; transgenic plant;
 XX Ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FH Misc-difference 7 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"
 FT Misc-difference 8 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000NO-US06759.
 XX
 XX 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX

XX
PI Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AIL protein with a mutation in the Rb binding region
XX
XX Claim 52: Page 45: 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AIL. AIL binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AIL
XX protein are used to produce transgenic plants. The mutation in AIL is
XX present in a ribosome binding region, and expression of mutant AIL
XX protein imparts increased resistance to geminivirus infection in the
XX plants. Transgenic plants with increased resistance to geminivirus infection as
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;

Query Match 91.3% Score 326; DB 21; Length 70;
Best Local Similarity 92.9% Pred. No. 5.3e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 TLVGEFQVDCRSARGSCOTSNDAAEALNASSKEALQITREKIPKYLFAFALNSNL 60
Db 1 TLVGEFQVDCRSARGSCOTSNDAAEALNASSKEALQITREKIPKYLFAFALNSNL 60
Oy 61 DRIFDKTPEP 70
Db 61 drifdktp 70

RESULT 8
AAB18690
ID AAB18690 standard; peptide: 70 AA.
XX
XX AAB18690;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AIL) protein.
XX
XX Geminivirus: replication protein; Rep protein; AIL: transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
XX Misc-difference 27 /note= "wild type residue replaced with Ala"
XX Misc-difference 30 /note= "wild type residue replaced with Ala"
XX W0200054573-A1.
XX 21-SEP-2000.
XX
XX 15-MAR-2000: 2000WO-US06759.
XX 18-MAR-1999: 99US-0125004.
XX 09-APR-1999: 99US-0289346.

XX
EA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AIL protein with a mutation in the Rb binding region
XX
XX Disclosure: Page 49: 73pp; English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AIL. AIL binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AIL
XX protein are used to produce transgenic plants. The mutation in AIL is
XX present in a ribosome binding region, and expression of mutant AIL
XX protein imparts increased resistance to geminivirus infection in the
XX plants. Transgenic plants with increased resistance to geminivirus infection as
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA;

Query Match 91.3% Score 326; DB 21; Length 70;
Best Local Similarity 92.9% Pred. No. 5.3e-34;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 TLVGEFQVDCRSARGSCOTSNDAAEALNASSKEALQITREKIPKYLFAFALNSNL 60
Db 1 TLVGEFQVDCRSARGSCOTSNDAAEALNASSKEALQITREKIPKYLFAFALNSNL 60
Oy 61 DRIFDKTPEP 70
Db 61 drifdktp 70

RESULT 9
AAB18678
ID AAB18678 standard; peptide: 70 AA.
XX
XX AAB18678;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AIL) protein.
XX Geminivirus: replication protein; Rep protein; AIL: transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Synthetic.
XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
XX Misc-difference 12 /note= "wild type residue replaced with Ala"
XX Misc-difference 13 /note= "wild type residue replaced with Ala"
XX Misc-difference 11 /note= "wild type residue replaced with Ala"
XX W0200054573-A1.
XX 21-SEP-2000.
XX

PF 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX containing a nucleic acid construct containing a nucleic acid sequence
 PI encoding a mutant A11 protein with a mutation in the RB binding region
 XX
 PT
 XX
 PS Claim 53: Page 42-43: 73pp: English.
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, bean dwarf mosaic virus, African cassava mosaic virus, bean golden mosaic
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX Sequence 70 AA:
 SQ
 Query Match 91.0%; Score 325; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 7.2e-34;
 Matches 64; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 TLVWGFQVDSRGSGCQTSNDAAAEALNASKEEALQIIREKIPKYLFAFALNSNL 60
 Db 1 TLVWGFQVDSRGSGCQTSNDAAAEALNASKEEALQIIREKIPKYLFAFALNSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 61 drifdktp 70
 RESULT 10
 AAB18686
 ID AAB18686 standard: peptide; 70 AA.
 AC AAB18686;
 XX 22-JAN-2001 (first entry)
 XX
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 DE Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX KEY Location/Qualifiers
 XX
 XX Misc-difference 24 /note= "wild type residue replaced with Leu"
 FT Misc-difference 25
 XX
 XX Misc-difference 26 /note= "wild type residue replaced with Leu"
 FT
 XX Misc-difference 27 /note= "wild type residue replaced with Leu"
 FT
 XX

PN W0200054573-A1.
 PD 21-SEP-2000.
 XX 15-MAR-2000: 2000MO-US06759.
 PR 09-APR-1999: 99US-0125004.
 XX 09-APR-1999: 99US-0289346.
 PR
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX containing a nucleic acid construct containing a nucleic acid sequence
 PI encoding a mutant A11 protein with a mutation in the RB binding region
 XX
 PT
 XX
 PS Claim 53: Page 46; 73pp: English.
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, bean dwarf mosaic virus, African cassava mosaic virus, bean golden mosaic
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX Sequence 70 AA:
 SQ
 Query Match 91.0%; Score 325; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 7.2e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 TLVWGFQVDSRGSGCQTSNDAAAEALNASKEEALQIIREKIPKYLFAFALNSNL 60
 Db 1 TLVWGFQVDSRGSGCQTSNDAAAEALNASKEEALQIIREKIPKYLFAFALNSNL 60
 Oy 61 DRIFDKTPEP 70
 Db 61 drifdktp 70
 RESULT 11
 AAB18689
 ID AAB18689 standard: peptide; 70 AA.
 AC AAB18689;
 XX 22-JAN-2001 (first entry)
 XX
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 DE Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX KEY Location/Qualifiers
 XX
 XX Misc-difference 22 /note= "wild type residue replaced with Ala"
 FT
 XX Misc-difference 23

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FT XX /note= "wild type residue replaced with Ala"
PX WO200054573-A1.
PD 21-SEP-2000.
PF 15-MAR-2000; 2000WO-US06759.
PX 18-MAR-1999; 90US-0125004.
PR 09-APR-1999; 99US-0289346.
PX (UYNC-) UNIV NORTH CAROLINA STATE.
PI Hanley-Bowdoin L, Orozco BM, Kong L;
DR WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprising a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
FT -
PX Disclosure: Page 48-49; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX cassava mosaic virus, squash leaf curl virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
XX
XX Query Match 90.8%; Score 324; DB 21; Length 70;
XX Best Local Similarity 92.9%; Pred. No. 9.5e-34;
XX Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 TLVGFQVQGRSGCGCTSDNDAAEALNASKEEALQIIREKIPKYLFAFAALNSL 60
DB 1 TLVGFQVQGRSGCGCTSDNDAAEALNASKEEALQIIREKIPKYLFAFAALNSL 60
OY 61 DRIFDKTPEP 70
DB 61 drifdktp 70
XX
XX RESULT 12
XX AAB18680
XX AAB18680 standard; peptide; 70 AA.
XX AC AAB18680;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance, geminivirus infection.
XX Synthetic.
XX OS Tomato golden mosaic virus.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 42

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FT XX /note= "wild type residue replaced with Ala"
PX WO200054573-A1.
PD 21-SEP-2000.
PF 15-MAR-2000; 2000WO-US06759.
PX 18-MAR-1999; 90US-0125004.
PR 09-APR-1999; 99US-0289346.
PX (UYNC-) UNIV NORTH CAROLINA STATE.
PI Hanley-Bowdoin L, Orozco BM, Kong L;
DR WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprising a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
FT -
XX Claim 52; Page 43-44; 73pp; English.
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein are used to produce transgenic plants. The mutation in AL1 is
XX present in a ribosome binding region, and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX cassava mosaic virus, squash leaf curl virus, bean golden mosaic
XX virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA;
XX
XX Query Match 90.2%; Score 322; DB 21; Length 70;
XX Best Local Similarity 91.4%; Pred. No. 1.7e-33;
XX Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 TLVGFQVQGRSGCGCTSDNDAAEALNASKEEALQIIREKIPKYLFAFAALNSL 60
DB 1 TLVGFQVQGRSGCGCTSDNDAAEALNASKEEALQIIREKIPKYLFAFAALNSL 60
OY 61 DRIFDKTPEP 70
DB 61 drifdktp 70
XX
XX RESULT 13
XX AAB18691
XX AAB18691 standard; peptide; 70 AA.
XX AC AAB18691;
XX
XX 22-JAN-2001 (first entry)
XX
XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX ribosome binding region; resistance, geminivirus infection.
XX Synthetic.
XX OS

```

OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 34 /note= "wild type residue replaced with Ala"
 FT Misc-difference 35 /note= "wild type residue replaced with Ala"
 FT Misc-difference 36 /note= "wild type residue replaced with Ala"
 FT Misc-difference 37 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 DR WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region
 XX Disclosure: Page 49; 73pp: English.
 XX The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. The A11 protein is present in a ribosome binding region, and expression of mutant A11 protein imparts increased resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 XX
 Query Match 90.2%; Score 322; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1.7e-33;
 Matches 64; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 TLVWGFVDCRSARGCCTSNDAAEALNASSKEALQIIREKIPKYPKYPALNLSN 60
 Db 1 TLVWGFVDCRSARGCCTSNDAAEALNASSKEALQIIREKIPKYPKYPALNLSN 60
 Oy 61 DRIFDKTPEP 70
 Db 61 drifdktp 70
 RESULT 14
 AAB18681
 ID AAB18681 standard: peptide: 70 AA.
 AC AAB18681;
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX

KW Geminivirus; replication protein; Rep protein; A11; transgenic plant; ribosome binding region; resistance; geminivirus infection.
 KW Synthetic.
 OS Tomato golden mosaic virus.
 PH Key Location/Qualifiers
 FT Misc-difference 47 /note= "wild type residue replaced with Ala"
 FT Misc-difference 48 /note= "wild type residue replaced with Ala"
 FT Misc-difference 49 /note= "wild type residue replaced with Ala"
 XX WO200054573-A1.
 XX 21-SEP-2000.
 XX 15-MAR-2000; 2000WO-US06759.
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 DR WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant A11 protein with a mutation in the Rb binding region
 XX Claim 52; Page 44; 73pp: English.
 XX The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as A11. A11 binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the A11 protein are used to produce transgenic plants. The mutation in A11 is present in a ribosome binding region, and expression of mutant A11 protein imparts increased resistance to geminivirus infection in the plant. Mutant A11 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 XX
 Query Match 89.4%; Score 319; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 4.1e-33;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 TLVWGFVDCRSARGCCTSNDAAEALNASSKEALQIIREKIPKYPKYPALNLSN 60
 Db 1 TLVWGFVDCRSARGCCTSNDAAEALNASSKEALQIIREKIPKYPKYPALNLSN 60
 Oy 61 DRIFDKTPEP 70
 Db 61 drifdktp 70
 RESULT 15
 AAB18683
 ID AAB18683 standard: peptide: 70 AA.
 XX AAB18683;
 XX

Job time: 154 sec

DT 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (Al1) protein.

XX KW Geminivirus: replication protein: Rep protein: Al1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 59 /note= "wild type residue replaced with Ala"

FT Misc-difference 61 /note= "wild type residue replaced with Ala"

FT Misc-difference 62 /note= "wild type residue replaced with Ala"

XX W02000054573-Al.

XX 21-SEP-2000.

XX 15-MAR-2000: 2000WO-US06755.

XX 18-MAR-1999: 99US-0125004.

XX 09-APR-1999: 99US-0289346.

XX (UYN-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX comprise a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant Al1 protein with a mutation in the Rb binding region

XX

XX Claim 53; Page 45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a

XX geminivirus replication (Rep) protein, also known as Al1. Al1 binds

XX to the 3' non-translated region (NTS) of single-stranded

XX DNA and interacts with the 3' NTS of the replicase. The Al1

XX protein is used to produce transgenic plants. The mutation in Al1 is

XX present in a ribosome binding region, and expression of mutant Al1

XX protein imparts increased resistance to geminivirus infection in the

XX plant. Mutant Al1 proteins are useful for producing plants having

XX increased resistance or reduced sensitivity to a geminivirus such as

XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX virus, bean dwarf mosaic virus, squash leaf curl virus, Indian

XX cassava mosaic virus, cotton leaf curl virus, Texas pepper

XX virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA;

Query Match 89.1%; Score 318; DB 21; Length 70;

Best Local Similarity 91.4%; Pos No 5, 5e-33;

Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TLWGEFQVDRGAGCQTNDAAEALNASKEEALQIREKIPKYLFAFAALNSNL 60

DB 1 tlvwgefvgdrgsarggcqtndaaeealnasskeaalqirekipekylfqlhlnsal 60

QY 61 DRIETKTEP 70

DB 61 aaifoktpep 70

1	340	95.2	352	1	VALLI_TGRV	P03567	tomato gold
2	240	67.2	361	1	VALLI_TPRV	P27256	potato yell
3	240	67.2	361	1	VALLI_TPRV	P27256	potato yell
4	227	63.6	358	1	VALLI_CUVN	P14372	cassava lat
5	220	61.6	362	1	VALLI_TYLCV	P36279	tomato yell
6	217	60.8	359	1	VALLI_TYLCV	P38609	tomato yell
7	210	58.8	359	1	VALLI_TYLCM	P27260	tomato yell
8	209	58.5	349	1	VALLI_PHVU	Q06923	pepper huas
9	204	57.1	353	1	VALLI_HGRV	P05175	bean golden
10	203	56.9	355	1	VALLI_HGRV	P21947	abutilon mon
11	200	56.0	358	1	VALLI_PCHV	P04451	beet curly
12	196	55.0	358	1	VALLI_PCHV	P04451	beet curly
13	191	53.5	357	1	VALLI_TYLCV	P27259	tomato yell
14	184	29.1	347	1	VALLI_SLCV	P29048	squash leaf
15	67	18.8	447	1	TUL22_HUMAN	Q094P3	homo sapien
16	64.5	18.1	1713	1	LMAS_HUMAN	Q16787	homo sapien
17	63.5	17.8	1610	1	CCAD_MESAU	Q09244	mesocricetu
18	63.5	17.8	2161	1	CCAD_HUMAN	Q01568	homo sapien
19	63.5	17.8	2203	1	CCAD_PANTR	P27372	rattus norv
20	63.5	17.8	2203	1	CCAD_PANTR	P27372	rattus norv
21	60	16.8	395	1	VALLI_TYDVA	P31817	saccharomyce
22	60	16.8	395	1	VALLI_TYDVA	P31817	saccharomyce
23	59.5	16.7	299	1	GRTE_RHOSH	P54305	rhodobacter
24	59.5	16.7	299	1	V175_RHEPJ	Q029q7	helicobacte
25	59.5	16.7	470	1	RHSA_RHIME	Q233r2	rhizobium u
26	59.5	16.7	4385	1	YF73_CABEL	Q09222	caenorhabdi
27	58.5	16.4	706	1	Y006_RICER	Q92ed6	rickettsia
28	58.5	16.4	132	1	Y005_CABEL	P34543	caenorhabdi
29	58.5	16.4	132	1	Y005_CABEL	P34543	caenorhabdi
30	58	16.2	447	1	CCSE_PROME	P56070	naemobacta
31	58	16.2	447	1	CCSE_PROME	P56070	naemobacta
32	57.5	16.1	367	1	LKCA_MOUSE	P33776	mus musculus
33	57.5	16.1	844	1	SRSA_STVCA	P47590	staphylococ
34	57.5	16.1	1852	1	CCV5_CYPCA	P23216	cyprinus car
35	57.5	16.1	1483	1	CCV1_YEAST	P1211	saccharomyce

ALIGNMENTS

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Db      171 DRFDKTEP 180
      RESULT 2
      VAL1 PYWV

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ID VALL_PYMVV STANDARD: PRT: 361 AA.
AC P27256;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE ALL PROTEIN: New mosaic virus (isolate Venezuela).
OS VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10828;
RN SEQUENCE FROM N.A.
RX MEDLINE=91311403; PubMed=1856690;
RA Coutts R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.:
RT The nucleotide sequence of the infectious cloned DNA components of
RI a new geminivirus, cassava latent virus DNA.
RI J. Gen. Virol. 72:1515-1520(1991).
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CC -----
DR EMBL: D00940; BAA0782.1;
DR FIRM: U0364; G007191; Geminiviridae; Geminiviruses;
DR PFAM: PF00759; Geminiviridae; Geminiviruses;
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCLVL.
DR PRODOM: PD000736; Geminiviridae; Geminiviruses;
DR ATP-binding: 222 228 ATP (POTENTIAL).
DR NP_BIND: 222 228
DR FT
DR SQ
Query Match 67.2%; Score 240; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 2e-19;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 TLWGEPVQDSRGAGCGTSDNDAEALNASKKEALQIIRKIPKYLFAFALNSL 60
DB 110 TIENGLFDLDSRGAGCGTSDNDAEALNASKKEALQIIRKIPKYLFAFALNSL 169
QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

QY 61 DRIFDKTPE 69
DB 170 DRIFDKAPE 178

RESULT 3
VALL_CLVSK
ID VALL_CLVSK STANDARD: PRT: 358 AA.
AC P14982;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 23, Last annotation update)
DE ALL PROTEIN (40.4 KDa PROTEIN).
OS Cassava latent virus (strain West Kenya 844).
OC VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10818;
RN SEQUENCE FROM N.A.
RX MEDLINE=90904919; PubMed=2309831;
RA Mott R., Coates L., Lowe S., Richardson K., Eddy P.:
RT "Nucleotide sequence of the infectious cloned DNA components of
RA African cassava mosaic virus (Nigerian strain)".
RT Nucleic Acids Res. 18:157-158(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC -----
DR EMBL: X17095; GAA34955.1;
DR FIRM: S07594; S07594
DR PFAM: PF00759; Geminiviridae; Geminiviruses;
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCLVL.
DR PRODOM: PD000736; Geminiviridae; Geminiviruses;
DR ATP-binding: 220 227 ATP (POTENTIAL).
DR NP_BIND: 220 227
DR SQ
Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 5.6e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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CC -----
DR EMBL: J02057; F000119; Geminiviridae; Geminiviruses;
DR FIRM: S07594; S07594
DR PFAM: PF00759; Geminiviridae; Geminiviruses;
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCLVL.
DR PRODOM: PD000736; Geminiviridae; Geminiviruses;
DR ATP-binding: 220 227 ATP (POTENTIAL).
DR NP_BIND: 220 227
DR SQ
Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 5.6e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 TLWGEPVQDSRGAGCGTSDNDAEALNASKKEALQIIRKIPKYLFAFALNSL 60
DB 109 TVWGCPFDLDSRGAGCGTSDNDAEALNASKKEALQIIRKIPKYLFAFALNSL 168
QY 61 DRIFDKTPE 70
DB 169 DRIFDEPPAP 178

RESULT 4
VALL_CLVN
ID VALL_CLVN STANDARD: PRT: 358 AA.
AC P14972;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUN-1994 (Rel. 23, Last annotation update)
DE ALL PROTEIN (40.4 KDa PROTEIN).
OS Cassava latent virus (strain Nigerian).
OC VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10819;
RN SEQUENCE FROM N.A.
RX MEDLINE=90904919; PubMed=2309831;
RA Mott R., Coates L., Lowe S., Richardson K., Eddy P.:
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)".
RT Nucleic Acids Res. 18:157-158(1990).
CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X17095; GAA34955.1;
DR FIRM: S07594; S07594
DR PFAM: PF00759; Geminiviridae; Geminiviruses;
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCLVL.
DR PRODOM: PD000736; Geminiviridae; Geminiviruses;
DR ATP-binding: 220 227 ATP (POTENTIAL).
DR NP_BIND: 220 227
DR SQ
Query Match 63.6%; Score 227; DB 1; Length 358;
Best Local Similarity 60.0%; Pred. No. 5.6e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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Oy 1 TLWGFEVQGRSARGCGQTSDNDAARALNASSKEPALQIREKIPKYLFAFALNSNL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 TVMGFOIDGRSAGQSDANTAKALNSGSALNVIHELVPDVIQVHMLNSNL 160
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 61 DRIFDKTPEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 DRIFQVPPAP 178
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
VAL1.TYLVCU
ID VAL1.TYLVCU STANDARD; PRT; 362 AA.
AC P36279;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
GN C1.
GS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36447;
RN J01887;
RP MEDLINE=93139778; PubMed=8423446;
RX Dry I.B., Ridgen J.E., Krake L.R., Mullineaux P.M., Rezaian M.A.;
RT "Nucleotide sequence and genome organization of tomato leaf curl
    Geminivirus."; 74:147-151(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
PR: J01887; J01887.
DR InterPro: IPR001191; Gemin1_A11.
DR Pfam: PF00799; Gemin1_A11; 1.
DR PRINTS; PR00227; GEMCOATALL.
DR PRINTS; PR00228; GEMCOATCLVL.
DR ProDom; PD000736; Gemin1_A11; 1.
KW ATP-binding. 221 228 ATP (POTENTIAL).
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 362 AA; 41197 MW; 343E7184B704098 CRC64;

Query Match
Best Local Similarity 61.6%; Score 220; DB 1; Length 362;
Matches 41; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

Oy 1 TLWGFEVQGRSARGCGQTSDNDAARALNASSKEPALQIREKIPKYLFAFALNSNL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLENGFEQIDGRSAGQSDANTAYAKALNSGSEALDYIKELAPRDYILHFNHNSNL 170
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 61 DRI-----FKTPE 69
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRITFPFLVNSPLSSSFDPVPE 194
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
VAL1.TYLVCU
ID VAL1.TYLVCU STANDARD; PRT; 359 AA.
AC P36609;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
GN C1.
GS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=37139;
RN J01887;
RP MEDLINE=94256836; PubMed=8198442;
RX Moris E., Hidalgo E., Accotto G., Moriones E.;
RT "High similarity among the tomato yellow leaf curl virus isolates
    from the west Mediterranean basin: the nucleotide sequence of an
    infectious clone from Spain.";

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Arch. Virol. 135:165-170(1994).
-1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC EMBL: S25751; G481026.1; -
CC PIRL: S39211; S39211.
CC InterPro: IPR001191; Gemin1_A11.
CC Pfam: PF00799; Gemin1_A11; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC PRINTS; PR00228; GEMCOATCLVL.
CC ProDom; PD000736; Gemin1_A11; 1.
KW ATP-binding. 221 228 ATP (POTENTIAL).
FT NP_BIND 221 228 ATP (POTENTIAL).
SQ SEQUENCE 359 AA; 41055 MW; 2D170A51EF60A3BC CRC64;

Query Match
Best Local Similarity 59.4%; Score 217; Length 359;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Oy 2 LWVGEFQVGRSARGCGQTSDNDAARALNASSKEPALQIREKIPKYLFAFALNSHL 61
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 111 LEMTQIDGRSAGCGQTANDAYAKALNSGSEALDYIKELAPRDYILHFNHNSNL 170
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 62 RIFDKTPEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 171 RVFQVPPAP 179
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
VAL1.TYLVCU
ID VAL1.TYLVCU STANDARD; PRT; 359 AA.
AC P27260;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE ALL PROTEIN (C1 PROTEIN).
GN C1.
GS Tomato yellow leaf curl virus (strain Marmande) (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10833;
RN J01887;
RP MEDLINE=92107600; PubMed=1840676;
RX Heyes Four A.; Benndorf M.; Matzelt V., Accotto G.P., Crepsl S.;
RX Gemin1_A11; 1.
RT "Tomato yellow leaf curl virus from Sardinia is a
    whitefly-transmitted monopartite geminivirus.";
RL Nucleic Acids Res. 19:6763-6769(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC EMBL: S251153; G481466.1; -
CC PIRL: S25593; S25593.
CC InterPro: IPR001191; Gemin1_A11.
CC Pfam: PF00799; Gemin1_A11; 1.
CC PRINTS; PR00227; GEMCOATALL.
CC PRINTS; PR00228; GEMCOATCLVL.
CC ProDom; PD000736; Gemin1_A11; 1.

```

KW ATP-binding. 220 227 ATP (POTENTIAL).
 FT NP_BIND 359 AA: 40733 MW: 9717BA07C93EFA7 CRC64;
 SQ SEQUENCE 359 AA: 40733 MW: 9717BA07C93EFA7 CRC64;
 Query Match 58.8%; Score 210; DB 1; Length 359;
 Best Local Similarity 56.5%; Pred. No. 4.4e-16;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
 OY 2 LVMGEFQVDSRGSGCCTSDNDAAEALNASSKEAALQITREKIPKYLFAFAALNSNL 61
 DB 111 LWMGEFQVDSRGSGCCTSDNDAAEALNASSKEAALQITREKIPKYLFAFAALNSNL 170
 OY 62 LRFQTKTPEP 70
 DB 171 KVFQVPPAP 179
 RESULT 8
 ID VALL_BGMV STANDARD; PRT; 349 AA.
 AC Q05923;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE ALL PROTEIN.
 OS ALL.
 GN Pepper huasteco virus (PHV).
 OC Viruses: sDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=28349;
 RN [1]
 RM SEQUENCE FROM N.A.
 RX MEDLINE=94015007; PubMed=8409944;
 RA Torres-Pacheco I., Garzon-Tiznado J.A., Herrera-Estrella L.,
 RA Rivera-Bustamante R.P.; Sequences of pepper huasteco virus: analysis and
 RA comparison with bipartite geminiviruses."
 RL J. Gen. Virol. 74:2225-2231(1993).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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 CC EMBL: X70418; CAA49856.1;
 DR PIR: S31875; S31875.
 DR TrEMBL: Q02303; P0001301;
 DR TrEMBL_P0001301; Geminiviridae; Geminiviridae; Geminiviridae; Geminiviridae;
 DR Pfam: PF00799; Geminiviridae; Geminiviridae; Geminiviridae; Geminiviridae;
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD000736; Geminiviridae; Geminiviridae; Geminiviridae; Geminiviridae;
 RN ATP-binding. 221 228 ATP (BY SIMILARITY).
 FT NP_BIND 349 AA: 39722 MW: D5FA76CD56370F4 CRC64;
 SQ SEQUENCE 349 AA: 39722 MW: D5FA76CD56370F4 CRC64;
 Query Match 58.5%; Score 209; DB 1; Length 349;
 Best Local Similarity 57.1%; Pred. No. 5.5e-16;
 Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
 OY 1 TLWGEFQVDSRGSGCCTSDNDAAEALNASSKEAALQITREKIPKYLFAFAALNSNL 60
 DB 110 TWGEFQVDSRGSGCCTSDNDAAEALNASSKEAALQITREKIPKYLFAFAALNSNL 169
 OY 61 DRIFDKTPEP 70
 DB 170 NRIFQTPPEP 179

RESULT 9
 ID VALL_BGMV STANDARD; PRT; 353 AA.
 AC P05175;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1995 (Rel. 34, Last annotation update)
 DE ALL PROTEIN (40.2 KDA PROTEIN).
 GN ACL.
 OS Bean golden mosaic virus.
 OC Viruses: sDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10839;
 RN [1]
 RM SEQUENCE FROM N.A.
 RA Howarth A.J., Caton J., Bossert M., Goodman R.M.;
 RA "Nucleotide sequence of bean golden mosaic virus and a model for gene
 RA regulation in geminiviruses."
 RT Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: M10070; AAA46318.1;
 DR InterPro: IPR001191; Geminiviridae; Geminiviridae; Geminiviridae; Geminiviridae;
 DR Pfam: PF00799; Geminiviridae; Geminiviridae; Geminiviridae; Geminiviridae;
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRODOM: PD000736; Geminiviridae; Geminiviridae; Geminiviridae; Geminiviridae;
 RN ATP-binding. 222 229 ATP (POTENTIAL).
 FT NP_BIND 353 AA: 40190 MW: 80FA779DF6029A34 CRC64;
 SQ SEQUENCE 353 AA: 40190 MW: 80FA779DF6029A34 CRC64;
 Query Match 57.1%; Score 204; DB 1; Length 353;
 Best Local Similarity 57.1%; Pred. No. 2e-15;
 Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;
 OY 1 TLWGEFQVDSRGSGCCTSDNDAAEALNASSKEAALQITREKIPKYLFAFAALNSNL 60
 DB 110 TWGEFQVDSRGSGCCTSDNDAAEALNASSKEAALQITREKIPKYLFAFAALNSNL 169
 OY 61 DRIFDKTPEP 70
 DB 170 NRIFQTPPEP 179
 RESULT 10
 ID VALL_BGMV STANDARD; PRT; 355 AA.
 AC P21947;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1995 (Rel. 29, Last annotation update)
 DE ALL PROTEIN.
 GN ACL.
 OS Abutilon mosaic virus (Isolate West India).
 OC Viruses: sDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10816;
 RN [1]
 RM SEQUENCE FROM N.A.
 RA Prischmuth T., Zimmet G., Jaske H.;
 RA "The nucleotide sequence of abutilon mosaic virus reveals prokaryotic
 RA as well as eukaryotic features."
 RT Virology 178:461-468(1990).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

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DR EMBL: X15983; ; NOT_ANNOTATED_CDS.
 DR PIR: A36214; OQCWMI.
 DR InterPro: IPR001191; Gemini_AL1.
 DR PIR: A36214; OQCWMI.
 DR PRINTS: PR00227; GEMCOATALL1.
 DR PRINTS: PR00228; GEMCOATCLVL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 DR ATP-Binding. 221 228 ATP (POTENTIAL).
 FT NP_BIND 221 228
 KW SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Best Local Similarity 56.9%; Score 203; DB 1; Length 355;
 Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Oy 1 TLVGFQVQDSARGCCQTSNDAAAEALNASKEEALQIIRKIPKYLFAFALNSL 60
 Db 110 TLVGFQVQDSARGCCQTSNDAAAEALNASKEEALQIIRKIPKYLFAFALNSL 169
 Oy 61 DRIFDKTPEP 70
 Db 170 ERIEFAKEP 179

RESULT 11
 ID VAL1_BCTV STANDARD; PRT; 358 AA.
 DT P14991;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE ALL PROTEIN (40.8 KDA PROTEIN).
 DE SwissProt: P14991; Gemini_AL1; 1.
 CC Viruses: SEDNA viruses, Geminiviridae; Curtovirus.
 CC NCBI_TaxID=10840;
 CC [1]

RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.:
 RP The nucleotide sequence of an infectious clone of the geminivirus
 RL Sweet curly top virus.
 RL Plant Dis. 71:176-178 (1986).

CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

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DR EMBL: X04144; ; NOT_ANNOTATED_CDS.
 DR InterPro: IPR001191; Gemini_AL1.
 DR PIR: A36214; OQCWMI.
 DR PRINTS: PR00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOATALL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 DR ATP-Binding. 222 229 ATP (POTENTIAL).
 FT NP_BIND 222 229
 KW SEQUENCE 358 AA; 40889 MW; 39A45E3C0B9C333 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 358;

Best Local Similarity 52.9%; Pred. No. 5.6e-15;
 Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
 Oy 1 TLVGFQVQDSARGCCQTSNDAAAEALNASKEEALQIIRKIPKYLFAFALNSL 60
 Db 110 TLVGFQVQDSARGCCQTSNDAAAEALNASKEEALQIIRKIPKYLFAFALNSL 169
 Oy 61 DRIFDKTPEP 70
 Db 170 OKIFRPPDP 179

RESULT 12
 ID VAL1_TMOV STANDARD; PRT; 361 AA.
 DT Q06657;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update).
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE ALL PROTEIN.

CC Tomato mottle virus (isolate Florida) (TMov).
 CC Viruses: SEDNA viruses; Geminiviridae; Begomovirus.
 CC NCBI_TaxID=36449;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=93107858; PubMed=1469361;
 CC Abouid A.M., Polston J.E., Hiebert E.;
 CC Isolated from tomato mottle virus, a new geminivirus
 CC isolated from tomato, Florida.
 CC J. Gen. Virol. 73:3225-3229 (1992).
 CC -!- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.

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DR EMBL: L14460; AAC32414.1; -.
 DR PIR: Q01677; TMOV.
 DR PIR: A36214; OQCWMI.
 DR PIR: A36214; OQCWMI.
 DR PIR: A36214; OQCWMI.
 DR PRINTS: PR00227; GEMCOATALL1.
 DR PRINTS: PR00228; GEMCOATCLVL1.
 DR ProDom: PD000736; Gemini_AL1; 1.
 DR ATP-Binding. 222 229 ATP (BY SIMILARITY).
 FT NP_BIND 222 229
 KW SEQUENCE 361 AA; 40516 MW; 8138B65CEEC950 CRC64;

Query Match 56.0%; Score 200; DB 1; Length 361;
 Best Local Similarity 52.9%; Pred. No. 5.7e-15;
 Matches 37; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Oy 1 TLVGFQVQDSARGCCQTSNDAAAEALNASKEEALQIIRKIPKYLFAFALNSL 60
 Db 110 TLVGFQVQDSARGCCQTSNDAAAEALNASKEEALQIIRKIPKYLFAFALNSL 169
 Oy 61 DRIFDKTPEP 70
 Db 170 ERIEFAKEP 179

RESULT 13
 ID VAL1_TYLCV STANDARD; PRT; 357 AA.
 DT P27259;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)

```

DE GN ALL PROTEIN (C1 PROTEIN).
OS C1.
OS Tomato yellow leaf curl virus (TYLCV).
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC [1] TaxID=10832.
RN SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RX Navot N., Pichersky E., Zeldan M., Zamir D., Czosnek H.;
RT "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT with a single genomic component.";
RL Virology 148:151-161(1991).
CC -----
CC [1] TaxID=10832; GEMINIVIRUSES ALL PROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X15655; CAA33688.1;
CC PIR: D40779; QQCVC1.
CC InterPro: IPR001191; Gemin_LAL1.
CC Pfam: PF00759; Gemin_LAL1.1.
CC PRINTS: PR00227; GEMCOATLVL1.
CC PROSITE: PR00228; GEMCOATLVL1.
CC PR000736; Gemin_LAL1.1.
CC ATP-binding; 219 226 ATP (POTENTIAL).
CC NP-BIND 219 226
CC SEQUENCE 357 AA; 40678 MW; 939A686E1AB3B2A7 CRC64;
CC -----
Query Match 53.5%; Score 191; DB 1; Length 357;
Best Local Similarity 62.8%; Pred. No. 5; ee 14;
Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
OY 4 WEEQVDSRGARGCGTSDNAAAEALNASKKEALQIREKIPKYLFAFALNSNLDRI 63
DB 111 FGVQIDGSRGARGCGQSANDAYAEALNASKSEALNLRKAPKDYLOFHLNSSLNDRI 170
OY 64 F 64
DB 171 F 171
RESULT 14
ID VALL_SLCV STANDARD; PRT; 347 AA.
CC 01-DEC-1992 (Rel. 24, Created)
CC 01-DEC-1992 (Rel. 24, Last sequence update)
CC 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALL PROTEIN.
OS Squash leaf curl virus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10829;
RN SEQUENCE FROM N.A.
RX MEDLINE=91082449; PubMed=1984668;
RX Lazarowitz S.G., Lazdins I.B.;
RT "Infectivity and complete nucleotide sequence of the cloned genomic
RT components of a bipartite squash leaf curl geminivirus with a broad
RT host range phenotype.";
RL Virology 140:39-68(1991).
CC -----
CC [1] TaxID=10829; GEMINIVIRUSES ALL PROTEIN FAMILY.
CC -----
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CC -----
CC EMBL: M39181; AAC2410.1; ALT7_INIT.
CC Title: 587/85; Gemin_LAL1.
CC Title: IPR001191; Gemin_LAL1.
CC Pfam: PF00759; Gemin_LAL1.1.
CC PRINTS: PR00227; GEMCOATLVL1.
CC PRINTS: PR00228; GEMCOATLVL1.
CC ProDom: PD000736; Gemin_LAL1.1.
CC ATP-binding; 218 225 ATP (POTENTIAL).
CC NP-BIND 218 225
CC SEQUENCE 347 AA; 39110 MW; AFDABDDDE122110E CRC64;
CC -----
Query Match 29.1%; Score 104; DB 1; Length 347;
Best Local Similarity 34.8%; Pred. No. 0.00025;
Matches 23; Conservative 14; Mismatches 25; Indels 4; Gaps 1;
OY 5 GFEQVDSRGARGCGTSDNAAAEALNASKKEALQIREKIPKYLFAFALNSNLDRI 64
DB 116 GQYKVGSG----GSKSNEDVYHNVAAGSGALDIIRKAGDPRTFYVHNLANVERLF 171
OY 65 DKTPPEP 70
DB 172 OKPPEP 177
RESULT 15
ID TBL2_HUMAN STANDARD; PRT; 447 AA.
CC 09V4P3; Q3UQE2;
CC 20-AUG-2001 (Rel. 40, Created)
CC 20-AUG-2001 (Rel. 40, Last sequence update)
CC 20-AUG-2001 (Rel. 40, Last annotation update)
DE TRANSDUCIN BETA-LIKE 2 PROTEIN (WS BETA-TRANSDUCIN REPEATS PROTEIN)
OS TBL2 (BETA-TRP).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN SCIENCE FROM N.A. PubMed=10575226;
RX MEDLINE=20044624;
RX Perez Jurado L.A., Wang Y.-K., Francke U., Cruces J.;
RT "TBL2, a novel transducin family member in the WBS deletion:
RT characterization of the complete sequence, genomic structure,
RT transcriptional variants and the mouse ortholog.";
RL Cytogenet. Cell Genet. 86:277-284(1999).
CC [1] TaxID=9606;
CC SCIENCE FROM N.A.
CC TBL2 (BETA-TRP).
CC TBL2_HUMAN.
RX MEDLINE=21154917; PubMed=11230166;
RX Wiemann S., Weill B., Wellenreuther R., Gassenhuber J., Glassl S.,
RX Ansoergo W., Bloeker M., Bloeker H., Bauersachs S., Blum H.,
RX Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RX Meves H.-W., Ottenwälder B., Obermaier B., Tampe J., Heubner D.,
RX Wambutt R., Korn B., Klein M., Poustka A.;
RX "Genomic structure and protein sequence analysis of the complete
RX analysis of 500 novel complete protein coding human (CDNAS).";
RL Genome Res. 11:422-435(2001).
CC [3]
CC SEQUENCE OF 14-447 FROM N.A.
CC MEDLINE=99075645; PubMed=9860302;
CC Meng X., Lu X., Li Z., Green E.D., Massa H., Trask B.J., Morris C.A.,
CC "Feeling the pain: a physical map of the common deletion region in Williams
CC syndrome and identification and characterization of three novel
CC genes.";
RL Hum. Genet. 103:590-595(1998).
CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
CC -----

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DR EMBL: AF097484; AAF06823.1; -;
 DR EMBL: AF097485; AAF06824.1; -;
 DR EMBL: AL080162; CAB45751.1; -;
 DR EMBL: AF056183; AAD28081.1; AUT_INIT.
 DR EMBL: AF056183; AAD28080.1; WD40.
 DR PIR: P00040; WD40.
 DR PRINTS: PR00320; GPROTEINERPT.
 DR SMART: SM00320; WD40: 5.
 DR PROSITE: PS00678; MD_REPEATS_1: 1.
 DR PROSITE: PS00682; MD_REPEATS_2: 3.
 DR PROSITE: PS0294; MD_REPEATS_REGION: 1.
 FT REPEAT: MD_REPEAT. 127 WD 1.
 FT REPEAT: 186 WD 2.
 FT REPEAT: 134 174 WD 3.
 FT REPEAT: 186 226 WD 4.
 FT REPEAT: 228 267 WD 5.
 FT REPEAT: 277 316 WD 6.
 FT REPEAT: 329 367 WD 7.
 FT REPEAT: 371 409 WD 8.
 FT REPEAT: 411 449 WD 9.
 SQ SEQUENCE 447 AA: 43797 MW: 8260087E1A71D3F9 CFC64;

Query Match 18.8% Score 67: DB 1; Length 447;
 Best Local Similarity 32.1%; Pred.No. 4.3;
 Matches 18; Conservative 11; Mismatches 23; Indels 4; Gaps 1;
 Qy 12 RSARGCQTSNDAAAEALMASSKEEAQIIRKIPKYLEAF----AALNSNLDRI 63
 Db 38 RSGRPACQKNGPPDPKSSGKQIQYQIRKXPQHNTHTLLAALKSHSNI 93

Search completed: January 3, 2002, 15:57:17
 Job time: 1103 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:56:25 ; Search time 131.69 seconds
(without alignments)
77.751 Million cell updates/sec

Title: US-09-289-346a-6

Perfect score: 357

Sequence: 1 TLVWGFQVDSARGGCGT.....FAFAALNSLDRIFDXTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 17.*

1: sp.archaea.*

2: sp.bacteria.*

3: sp.fungi.*

4: sp.human.*

5: sp.invertebrate.*

6: sp.mammal.*

7: sp.mic.*

8: sp.organelle.*

9: sp.phase.*

10: sp.plant.*

11: sp.podent.*

12: sp.virus.*

13: sp.yeast.*

14: sp.unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	289	81.0	352	12 Q9E000	Q9E000 tomato psu
2	272	76.2	226	12 Q09727	Q09727 leonurus mo
3	272	76.2	226	12 Q9H76	Q9H76 tomato mild
4	270	75.6	351	12 Q67574	Q67574 bean golden
5	268	75.1	314	12 Q9E178	Q9E178 cowpea gold
6	268	75.1	314	12 Q9E178	Q9E178 cowpea gold
7	268	75.1	314	12 Q9E555	Q9E555 sweet potato
8	265	74.2	165	12 Q9E693	Q9E693 sida golden
9	257	72.0	149	12 P88975	P88975 macroptiliu
10	257	72.0	149	12 Q9YL44	Q9YL44 macroptiliu
11	251	70.3	233	12 Q39180	Q39180 potato yell
12	248	69.5	190	12 Q9Z089	Q9Z089 tobacco lea
13	247	69.5	190	12 Q9Z089	Q9Z089 tobacco lea
14	247	69.5	190	12 Q9Z089	Q9Z089 tobacco lea
15	247	69.2	208	12 Q9Z0C4	Q9Z0C4 tobacco lea
16	245	68.6	208	12 Q9Z0C0	Q9Z0C0 tobacco lea
17	245	68.6	208	12 Q9Z0B8	Q9Z0B8 tobacco lea
18	243	68.1	208	12 Q9Z0B6	Q9Z0B6 tobacco lea
19	242	67.8	203	12 Q9Z0B3	Q9Z0B3 tobacco lea

ALIGNMENTS

RESULT 1
ID Q9E000 PRELIMINARY: PRT; 352 AA.
OC Q9E000: 2001 (TREMBL) 15. Created)
AC Q9E000: 2001 (TREMBL) 15. Last sequence update)
DT 01-MAR-2001 (TREMBL) 15. Last sequence update)
DT 01-JUN-2001 (TREMBL) 17. Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN.
GN AC1.

OS Tomato ruose mosaic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
SM NCBI_TaxID=134599;

RA SEQUENCE FROM N.A.
RP Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,

RA Zambolim E.M., Zerbini F.M.;

RA *Molecular Cloning and Characterization of Tomato ruose mosaic virus

(TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro,

RT Minas Gerais, Brazil.;

RT Submitted (JUL-2000) to GenBank/EMBL/

RL GenBank accession number: AF0001191

TR: PRT; IP: 0001191; Geminiviridae.

DR PFAM: PF00759; Geminiviridae.

DR PRINTS: PR00227; GEMCOATALL.

DR Problem: PD000736; Geminiviridae.

SQ SEQUENCE 352 AA; 40012 MW; 17CD55638E24D613 CRC64;

Query Match 81.0%; Score 289; DB 12; Length 352;

Best Local Similarity 76.6%; Pred. No. 1,6e+24;

Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 TLVWGFQVDSARGGCGTSDAAEAALNSKREALQITREKIPKIFAFALNSNL 60

! : !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!! !!!!!!!

DB 111 TTEMCEPQIDGSRGCGGTANDAAEAALNSKREALQITREKIPKIFAFALNSNL 170

QY 61 DRIEKTPEP 70

DB 171 DRIEKTPEP 180

RESULT 2

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009727
ID 009727 PRELIMINARY; PRT: 226 AA.
AC Q5WHF6;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE 1 TWVGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 170
DE REP PROTEIN (FRAGMENT)..
GN Leonurus mosaic virus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=58177;
RN [1]
RC SEQUENCE FROM N.A.
RA Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U92532; AAB51157.1;
DR InterPro: IPR001191; Gemin_ALI.
DR Pfam: PF00799; Gemin_ALI.1.
DR PRINTS: PR00227; GEMCONVALI.
DR PRODOM: PD000736; Gemin_ALI.1.
DR NCBI_TaxID=226;
PT NON_TER
SQ SEQUENCE 226 AA: 22617 MW: 73CDBE6766083FC5 CRC64;

Query Match 76.2%; Score 272; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 7.8e-23;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 60
Db 111 TVMGEFQVDSRGSGCQTNDAAAEALNAPDKRTALQIILKEKLPKFLFOYHNLSNL 170

Qy 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 3
ID Q5WHF6 PRELIMINARY; PRT: 226 AA.
AC Q5WHF6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 1 TWVGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 170
DE REP PROTEIN (FRAGMENT)..
GN Leonurus mosaic virus.
OS Viruses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
OC NCBI_TaxID=52943;
RN [1]
RC SEQUENCE FROM N.A.
RA Nakhla M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M., Maxwell D.P.;
RL "Molecular characterization and DNA-based detection methods for vegetable-infecting geminiviruses in Central America.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF137933; Gemin_ALI.1.
DR InterPro: IPR001191; Gemin_ALI.
DR Pfam: PF00799; Gemin_ALI.1.
DR PRINTS: PR00227; GEMCONVALI.
DR PRODOM: PD000736; Gemin_ALI.1.
DR NCBI_TaxID=226;
PT NON_TER
SQ SEQUENCE 226 AA: 225941 MW: 2EAM116712871A23 CRC64;

Query Match 76.2%; Score 272; DB 12; Length 226;
Best Local Similarity 72.9%; Pred. No. 7.8e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TLVGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 60
Db 111 TVMGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 170

Qy 61 DRIFDKTPEP 70
Db 171 DRIFAKAPEP 180

RESULT 4
ID Q67574 PRELIMINARY; PRT: 361 AA.
AC Q67574;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 1 TWVGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 170
DE REP PROTEIN (FRAGMENT)..
GN PUTATIVE REPLICATIVE PROTEIN.
OS Bean golden mosaic virus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=10839;
RN [1]
RC SEQUENCE FROM N.A.
RA Morales F.J., Russell D.R.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL: M88686; AAA6312.1;
DR InterPro: IPR001191; Gemin_ALI.
DR Pfam: PF00799; Gemin_ALI.1.
DR PRINTS: PR00227; GEMCONVALI.
DR PRODOM: PD000736; Gemin_ALI.1.
DR NCBI_TaxID=361;
PT NON_TER
SQ SEQUENCE 361 AA: 41041 MW: 0094C7ACAF06B788 CRC64;

Query Match 75.6%; Score 270; DB 12; Length 361;
Best Local Similarity 76.1%; Pred. No. 2.3e-22;
Matches 51; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 4 WGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNLDRI 63
Db 113 WGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNLDRI 172

Qy 64 FDKTPEP 70
Db 173 FTRADP 179

RESULT 5
ID Q5QDB1 PRELIMINARY; PRT: 225 AA.
AC Q5QDB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 1 TWVGEFQVDSRGSGCQTNDAAAEALNASSKEAMRIIKEKLPKFLFOYHNLSNL 170
DE REP PROTEIN (FRAGMENT)..
GN cowpea golden mosaic geminivirus.
OS Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxID=69263;
RN [1]
RC SEQUENCE FROM N.A.
RA Faria J.C.;
RL "Partial nucleotide sequence of cowpea golden mosaic geminivirus from Brazil.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF188708; AAF06318.1; -.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOVAL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 FT NON_TER 225 AA; 225
 SQ SEQUENCE 225 AA; 225/66 MW; 1089CB60BD15B5D CRC64;

Query Match 75.1% Score 268; DB 12; Length 225;
 Best Local Similarity 76.1%; Pred. No. 2.2e-22;
 Matches 54; Conservative 8; Mismatches 0; Gaps 0;
 QY 4 TWGGEFQVDSRGSGCOTSDNDAAALNASSKEALQITREKIPKYLFAFAALNSNL 63
 DB 113 WGHFQIDRSARGGQOTINDAAALNASSKEALQITREKIPKYLFAFAALNSNL 172

QY 64 FKPTPEP 70
 DB 173 FKPTPEP 179

RESULT 6
 ID 095L78 PRELIMINARY; PRT: 314 AA.
 AC 095L78; 2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
 DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATION PROTEIN.
 GN AC1.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

QX NCBI_TaxID=100755;
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RA "Detection of a geminivirus infecting sweet potato in the United States."
 RT Plant Dis. 82:1253-1257 (1998).
 RN [2]
 RC SEQUENCE FROM N.A.
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RI EMBL: AF288227; MAG1006.1; -.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOVAL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 314 AA; 3315 MW; 6B5220613046943F CRC64;

Query Match 75.1% Score 268; DB 12; Length 314;
 Best Local Similarity 79.4%; Pred. No. 3.2e-22;
 Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 1 TLWGEFQVDSRGSGCOTSDNDAAALNASSKEALQITREKIPKYLFAFAALNSNL 60
 DB 110 TITWGEFQVDSRGSGCOTSDNDAAALNASSKEALQITREKIPKYLFAFAALNSNL 169

QY 61 DRIFDKTP 68
 DB 170 DRIFDKTP 177

RESULT 7
 ID 090S55 PRELIMINARY; PRT: 364 AA.
 AC 090S55;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN AC1.

GN AC1.
 OS sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 QX NCBI_TaxID=100755;
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RA "Detection of a geminivirus infecting sweet potato in the United States."
 RT Plant Dis. 82:1253-1257 (1998).
 RL EMBL: AF104036; AD47173.1; -.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOVAL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 SQ SEQUENCE 364 AA; 40680 MW; 5F79752431A09D5E CRC64;

Query Match 75.1% Score 268; DB 12; Length 364;
 Best Local Similarity 79.4%; Pred. No. 3.8e-22;
 Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSRGSGCOTSDNDAAALNASSKEALQITREKIPKYLFAFAALNSNL 60
 DB 110 TITWGEFQVDSRGSGCOTSDNDAAALNASSKEALQITREKIPKYLFAFAALNSNL 169

QY 61 DRIFDKTP 68
 DB 170 DRIFDKTP 177

RESULT 8
 ID 098693 PRELIMINARY; PRT: 185 AA.
 AC 098693; 1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REP PROTEIN (FRAGMENT).
 GN AC1.
 OS sida golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

QX NCBI_TaxID=51034;
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RA "Detection of a geminivirus infecting sweet potato in the United States."
 RT Plant Dis. 82:1253-1257 (1998).
 RN [2]
 RC SEQUENCE FROM N.A.
 RL Plant Dis. 81:1251-1258 (1997).
 RI EMBL: U67926; AAB97865.1; -.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1; 1.
 DR PRINTS: PR00227; GEMCOVAL1.
 DR PRODOM: PD000736; Gemini_AL1; 1.
 FT NON_TER 185
 SQ SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CRC64;

Query Match 74.2% Score 265; DB 12; Length 185;
 Best Local Similarity 70.0%; Pred. No. 3.8e-22;
 Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLWGEFQVDSRGSGCOTSDNDAAALNASSKEALQITREKIPKYLFAFAALNSNL 60
 DB 89 TIEWGVFQIDRSARGGQOTINDAAALNASSKEALQITREKIPKYLFAFAALNSNL 148

QY 61 DRIFDKTP 70
 DB 149 DRIFDKTP 158

RESULT 9
 P88975

ID P88975 PRELIMINARY: PRT: 149 AA.
 AC 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN ACP.
 OS Macrotipium golden mosaic geminivirus.
 OC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51576;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA ROY M.E., McLaughlin W.A., Maxwell D.P.,
 RL Thesis (1996), Biochemistry, University of the West Indies, Jamaica.
 RL EMBL: U75278; AAB36919.1; -.
 AC 039180 PRELIMINARY: PRT: 234 AA.
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN InterPro: PF00799; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCONTAL1.
 DR PRODOM: PD000736; GEMCONTAL1.
 DR PRODOM: PD000736; GEMCONTAL1.
 FT NON_TER 149 149
 SQ SEQUENCE 149 AA: 16785 MW; EACF5ED4C9CD508 CRC64;

Query Match 72.0%; Score 257; DB 12; Length 149;
 Best Local Similarity 68.6%; Pred. No. 2.3e-21;
 Matches 46; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 TLWGFQVDRSANGCQTSNDAAAEALNASSKEAALTIIRKIPKYLFAFAALNSNI 60
 Db 52 TIENGVFQIDRSANGCQTSNDAAAEALNASSKEAALHIVKELPEKLFQYHNLSSNL 111
 Oy 61 DRIFDKTPPEP 70
 Db 112 DRIFMKPPEP 121
 RESULT 10
 ID 09YL44 PRELIMINARY: PRT: 233 AA.
 AC 09YL44: 1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Macrotipium golden mosaic geminivirus.
 OC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
 OX NCBI_TaxID=51676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA ROY M.E.,
 RL STRAIN-JAMAICA STRAIN 1;
 RA ROY M.E.;
 RL "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses
 RL Submitted (Oct-1998) to the EMBL/Genbank/DBSJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA STRAIN-JAMAICA STRAIN 1;
 RA ROY M.E., McLaughlin W.A., Maxwell D.P.;
 RL "Molecular characterization of two distinct geminiviruses infecting M.
 RL lathyrus from Jamaica.";
 RL Submitted (Oct-1998) to the EMBL/Genbank/DBSJ databases.
 RL EMBL: AF098940; AAD17850.1; -.
 DR InterPro: IPR001191; Gemini_AL1.
 DR PRINTS: PR00227; GEMCONTAL1.
 DR PRODOM: PD000736; Gemini_AL1.
 DR PRODOM: PD000736; Gemini_AL1.
 FT NON_TER 233 233
 SQ SEQUENCE 233 AA: 26355 MW; AA490AF4D2166A02 CRC54;

Query Match 72.0%; Score 257; DB 12; Length 233;
 Best Local Similarity 68.6%; Pred. No. 3.9e-21;
 Matches 46; Conservative 12; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 TLWGFQVDRSANGCQTSNDAAAEALNASSKEAALTIIRKIPKYLFAFAALNSNI 60
 Db 110 TIENGVFQIDRSANGCQTSNDAAAEALNASSKEAALHIVKELPEKLFQYHNLSSNL 169
 Oy 61 DRIFDKTPPEP 70
 Db 170 DRIFMKPPEP 179
 RESULT 11
 ID 039180 PRELIMINARY: PRT: 234 AA.
 AC 039180:
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.
 DR PRINTS: PR00227; GEMCONTAL1.
 DR PRODOM: PD000736; Gemini_AL1.
 DR PRODOM: PD000736; Gemini_AL1.
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA: 26486 MW; 9ED8F0697105CD19 CRC64;

Query Match 70.3%; Score 251; DB 12; Length 234;
 Best Local Similarity 67.1%; Pred. No. 1.9e-20;
 Matches 47; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 TLWGFQVDRSANGCQTSNDAAAEALNASSKEAALTIIRKIPKYLFAFAALNSNI 60
 Db 110 TIENGVFQIDRSANGCQTSNDAAAEALNASSKEAALHIVKELPEKLFQYHNLSSNL 169
 Oy 61 DRIFDKTPPEP 70
 Db 170 DRIFMKPPEP 179
 RESULT 12
 ID 09Z089 PRELIMINARY: PRT: 190 AA.
 AC 09Z089:
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CL1 AND C4 GENES; CLONE YOKOHAMA3-1, PARTIAL AND COMPLETE CDS
 GN C4 (FRAGMENT).
 OS tobacco leaf curl virus.
 OC Viruses: ssDNA viruses: Geminiviridae; Begomovirus.
 OX NCBI_TaxID=67762;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA STRAIN-YOKOHAMA3;
 RL "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
 RL J. Plant Res. 110:247-257 (1997).
 RL EMBL: AB001315; BAA34033.1; -.
 DR InterPro: IPR001191; Gemini_AL1.
 DR Pfam: PF00799; Gemini_AL1.

DR PRINTS: PR00227; GEMCORTALL1.
 DR PRODOM: PD000736; Gemin1_ALL; 1.
 FT NON_TER 190 1
 FT SEQUENCE 190 AA; 21432 MW; AACU093DD1610FAD CRC64;
 SQ SEQUENCE 190 AA; 21432 MW; AACU093DD1610FAD CRC64;

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.5%; Score 248; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 3.2e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

OX NCBI_TaxID=67762;
 RN SEQUENCE FROM N.A.
 RP STRAIN=KOKOHAMA5;
 PA Ooi K., Ohshita S., Ishii I., Yahara T.;
 "Molecular phylogeny of geminivirus infecting wild plants in Japan.";
 J. Plant Res. 110:247-257(1997).
 RL EMBL; AB001303; BAA34010.1; -;
 DR InterPro; IPR001191; Gemin1_ALL.
 DR Pfam; PF00799; Gemin1_ALL; 1.
 DR PRINTS; PR00227; GEMCORTALL1.
 DR PRODOM; PD000736; Gemin1_ALL; 1.
 FT NON_TER 190 190
 FT SEQUENCE 190 AA; 21444 MW; 93C3742A8EBD7EB CRC64;

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Query Match 69.2%; Score 247; DB 12; Length 190;
 Best Local Similarity 58.8%; Pred. No. 4.1e-20;
 Matches 50; Conservative 8; Mismatches 11; Indels 16; Gaps 1;

Oy 1 TLVNGCFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 60
 DB 85 TLENGTFQVDSRGSGCOTNSDAAEALNASSKEEALQITREKIPKYLFAFALNSNL 144
 Oy 61 DRI-----FQKTP 69
 DB 145 DRIAPFLEVPCTASSFDQVPE 169

Search completed: January 3, 2002, 15:56:25

Job time: 1121 sec

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OW protein - protein search, using sw model

Run on: January 3, 2002, 15:38:50 : Search time 65.28 Seconds
(without alignments)
24,130 Million cell updates/sec

Title: US-09-289-346A-6

Perfect score: 357

Sequence: 1 TLWGEFQVDSARGCQT.....FAFAALNSLDRFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212532 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents JA.*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/1aa/PTCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/1aa/bcckilles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	210	58.8	359	4	US-08-809-103B-2
2	210	58.8	359	4	US-08-809-103B-4
3	210	58.8	359	4	US-08-809-103B-6
4	210	58.8	359	4	US-08-809-103B-8
5	206	57.7	333	4	US-08-838-151A-4
6	206	57.7	333	4	US-08-838-151A-6
7	206	57.7	333	4	US-08-838-151A-8
8	206	57.7	333	4	US-08-838-151A-10
9	206	57.7	333	4	US-08-838-151A-12
10	204	57.1	361	4	US-08-838-151A-14
11	204	57.1	361	4	US-08-838-151A-16
12	204	57.1	361	4	US-08-838-151A-18
13	194	57.1	361	4	US-08-838-151A-20
14	194	57.1	361	4	US-08-838-151A-22
15	191	53.5	357	4	US-08-838-151A-24
16	191	53.5	357	4	US-08-838-151A-26
17	183	51.3	357	4	US-08-838-151A-28
18	64.5	18.1	1713	3	US-08-600-982-24
19	64.5	18.1	1713	5	PCR-US94-102G1A-24
20	63.5	17.8	2161	1	US-07-745-206A-2
21	63.5	17.8	2161	1	US-08-453-543A-51
22	63.5	17.8	2161	1	US-08-223-305C-49
23	63.5	17.8	2161	2	US-08-223-305C-51
24	63.5	17.8	2161	2	US-08-311-363-2
25	63.5	17.8	2161	2	US-08-838-151A-14
26	60.5	16.9	131	4	US-08-838-151A-16
27	58	16.2	446	2	US-08-672-814D-11

28 58 16.2 446 4 US-09-333-696-11
29 55.5 15.5 593 4 US-09-234-393-54
30 55 15.4 374 4 US-09-091-405-2
31 55 15.3 395 2 US-09-011-669-13
32 54.5 15.3 395 2 US-09-011-669-13
33 54 15.1 633 1 US-08-458-477A-5
34 54 15.1 633 1 US-09-033-153-5
35 54 15.1 633 4 US-09-325-430B-5
36 54 15.1 765 2 US-08-663-112-2
37 53.5 15.0 217 1 US-08-621-081A-23
38 53.5 15.0 593 4 US-09-234-393-24
39 53.5 15.0 593 4 US-09-234-393-26
40 53.5 15.0 593 4 US-09-234-393-28
41 53 14.8 266 2 US-07-857-224B-40
42 53 14.8 374 2 US-08-928-692-51
43 53 14.8 454 3 US-08-446-100-30
44 52.5 14.7 217 1 US-08-621-081A-22
45 52.5 14.7 382 2 US-08-477-451-28

ALIGNMENTS

RESULT 1
US-08-809-103B-2
: Sequence 2, Application US/08809103B
: Patent No. 6133505
: GENERAL INFORMATION:
: TITLE OF INVENTION: PHOTOPATHOGENIC DNA VIRUS
: TITLE OF INVENTION: PHOTOPATHOGENIC DNA VIRUS RESISTANT
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Wisconsin
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: GENCOM, Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/809,103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PCT APPLICATION DATA:
: APPLICATION NUMBER: NO PCT/FR95/01192
: FILING DATE: 15-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PATCH, Andrew J.
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: US94AL CNR TOM
: TELECOMMUNICATIONS INFORMATION:
: TELEPHONE: (703) 685-0577
: TELEFAX: (703) 685-0573
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 359 amino acids
: TYPE: amino acid
: MOLECULE TYPE: protein
US-08-809-103B-2

Query Match 58.8%; Score 210; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 2.8e-20;

Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFVDGSRGCGQTSDNDAARALNASSKEALQIREKIPKYLFAFALNSLMD 61
 DB 111 LKMGTFQIDGSRGCGQTANDAYAKANAGSKSQALDVIKELAPROYVLHFNHNSLMD 170

QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 2
 US-08-809-103B-4
 : Sequence 4, Application US/08809103B
 : Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GORENBORN, Bruno
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: YOUNG & THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION NUMBER: US/08/809.103B
 : FILING DATE: 17-MAR-1997
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: FR 94.11040
 : FILING DATE: 15-SEP-1994
 : PRIOR APPLICATION NUMBER: NO PCT/FR95/01192
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PATCH, Andrew J.
 : REGISTRATION NUMBER: 32.925
 : REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 521-2297
 : TELEFAX: 248425 EMBON
 : TELEX: 248425 EMBON
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 359 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-809-103B-4

Query Match 58.8%; Score 210; DB 4; Length 359;
 Best Local Similarity 56.5%; Pred. No. 2.8e-20;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFVDGSRGCGQTSDNDAARALNASSKEALQIREKIPKYLFAFALNSLMD 61
 DB 111 LKMGTFQIDGSRGCGQTANDAYAKANAGSKSQALDVIKELAPROYVLHFNHNSLMD 170

QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 3

US-08-809-103B-6
 : Sequence 6, Application US/08809103B
 : Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GORENBORN, Bruno
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: YOUNG & THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION NUMBER: US/08/809.103B
 : FILING DATE: 17-MAR-1997
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: FR 94.11040
 : FILING DATE: 15-SEP-1994
 : PRIOR APPLICATION NUMBER: NO PCT/FR95/01192
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PATCH, Andrew J.
 : REGISTRATION NUMBER: 32.925
 : REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 521-2297
 : TELEFAX: 248425 EMBON
 : TELEX: 248425 EMBON
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 359 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-809-103B-6

Query Match 58.8%; Score 210; DB 4; Length 359;
 Best Local Similarity 56.5%; Pred. No. 2.8e-20;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LVWGEFVDGSRGCGQTSDNDAARALNASSKEALQIREKIPKYLFAFALNSLMD 61
 DB 111 LKMGTFQIDGSRGCGQTANDAYAKANAGSKSQALDVIKELAPROYVLHFNHNSLMD 170

QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 4
 US-08-809-103B-8
 : Sequence 8, Application US/08809103B
 : Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GORENBORN, Bruno
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: YOUNG & THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington


```

;
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

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Query Match      57.7%: Score 206; DB 4; Length 353;
Best Local Similarity 57.1%; Pred No. 1.8e-19;
Matches 40; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

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Oy 1 TLVWGFQVQDSARGCGCTSNDAALNASKEALQIREKIPKYLFAFALNSNL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIENGFOFQDSARGCGOOSANDSYAKALNADSTESALTILKEOPADYVLQHNIRSNL 169

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Oy 61 DRIFDKTPEP 70
Db 170 ERIFVWKEP 179

RESULT 10
; Sequence 2, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Slout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiviruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A

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; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-2

Query Match      57.1%: Score 204; DB 4; Length 361;
Best Local Similarity 54.3%; Pred No. 1.8e-19;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

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Oy 1 TLVWGFQVQDSARGCGCTSNDAALNASKEALQIREKIPKYLFAFALNSNL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TIENGFOFQDSARGCGOOSANDSYAKALNADSTESALTILKEOPADYVLQHNIRSNL 169

Oy 61 DRIFDKTPEP 70
Db 170 ERIFVWKEP 179

RESULT 11
; Sequence 4, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Slout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiviruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-838-151A-4

Query Match 57.1%; Score 204; DB 4; Length 361;
 Best Local Similarity 54.3%; Pred. No. 1.8e-19;
 Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGSCGTSDNAAAEALNASSKEDEALOTIREKIPKYLFAFALNSNL 60
 DB 110 TIENGDFQDSARGSCQSDSYAKALNASSVSALAVIREQPKDFVLQNHNI RSNL 169

QY 61 DRIFDKPTPE 70

DB 170 ERIFAKAPEP 179

RESULT 12

US-08-838-151A-6

: Sequence 6, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Luu, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : FILING DATE: NUMBER: US/08/838,151A
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mueller, Lisa V
 : REGISTRATION NUMBER: 38,978
 : REFERENCE/DOCKET NUMBER: SVS3801P0260
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 361 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-838-151A-6

Query Match 57.1%; Score 204; DB 4; Length 361;
 Best Local Similarity 54.3%; Pred. No. 1.8e-19;
 Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGSCGTSDNAAAEALNASSKEDEALOTIREKIPKYLFAFALNSNL 60
 DB 110 TIENGDFQDSARGSCQSDSYAKALNASSVSALAVIREQPKDFVLQNHNI RSNL 169

QY 61 DRIFDKPTPE 70

DB 170 ERIFAKAPEP 179

RESULT 13

US-08-838-151A-8

: Sequence 8, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Luu, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/838,151A
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mueller, Lisa V
 : REGISTRATION NUMBER: 38,978
 : REFERENCE/DOCKET NUMBER: SVS3801P0260
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 361 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-838-151A-8

Query Match 57.1%; Score 204; DB 4; Length 361;

Best Local Similarity 54.3%; Pred. No. 1.8e-19;
 Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 TLVWGEFQVDSARGSCGTSDNAAAEALNASSKEDEALOTIREKIPKYLFAFALNSNL 60
 DB 110 TIENGDFQDSARGSCQSDSYAKALNASSVSALAVIREQPKDFVLQNHNI RSNL 169

QY 61 DRIFDKPTPE 70

DB 170 ERIFAKAPEP 179

RESULT 14

US-08-838-151A-24

: Sequence 24, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Luu, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:

```

: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Ill.
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE: US/83601P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 357 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-838-151A-24

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Query Match 53.5%; Score 191; DB 4; Length 357;

Best Local Similarity 62.3%; Pred. No. 1e-17; Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

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Qy 4 WGEFVDGSRGSGCOTSDAAAEALNASSKKEEALOTIREKIPKYLEFAPALNSNLDRI 63
Db 111 FGVSDIGSRGSGQOSANDAYAEALNSGSKSEALNLKEKAPKDYILQPHNLSNLDRI 170
Qy 64 F 64
Db 171 F 171

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RESULT 15

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: US-08-838-151A-27
: Sequence 27, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Liu, Jiang
: APPLICANT: Knebel, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CONGRESS/SEQUENCE ADDRESS:
: CONGRESS/SEQUENCE ADDRESS: Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800

```

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: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE: US/83601P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 357 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-838-151A-27

```

Query Match 53.5%; Score 191; DB 4; Length 357;

Best Local Similarity 62.3%; Pred. No. 1e-17; Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

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Qy 4 WGEFVDGSRGSGCOTSDAAAEALNASSKKEEALOTIREKIPKYLEFAPALNSNLDRI 63
Db 111 FGVSDIGSRGSGQOSANDAYAEALNSGSKSEALNLKEKAPKDYILQPHNLSNLDRI 170
Qy 64 F 64
Db 171 F 171

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Search completed: January 3, 2002, 15:38:50

Job time: 227 sec

GenCode version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:10 ; Search time 72.79 Seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346A-6

Perfect score: 357

Sequence: 1 TLVNGEFQVDSARGGCGT.....FAFAALNSLDRFDKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	340	95.2	1	352	1 QOCVLI	AlI protein - toma
2	240	67.2	361	1	QOCVLI	AlI protein - toma
3	227	63.6	358	2	S07594	hypothetical prote
4	220	61.6	362	1	JQ1887	AlI protein - toma
5	217	60.8	359	2	S39211	gene Cl protein -
6	212	59.4	351	2	J02327	AlI protein - indi
7	209	58.6	350	2	S22533	hypothetical prote
8	209	58.5	350	2	S22533	hypothetical prote
9	209	58.5	349	2	S31875	AlI protein - pep
10	204	57.1	359	2	S39235	gene Cl protein -
11	203	56.9	355	1	QOCVM1	AVI protein - abut
12	200	56.0	358	1	JQ1870	AlI protein - toma
13	200	56.0	385	2	S28360	replication-associ
14	193	54.1	360	2	S59885	AlI protein - toma
15	193	54.1	360	2	S59885	AlI protein - toma
16	116	33.1	131	1	S45059	AlI protein - aqua
17	104	29.1	347	1	QOCVSI	AlI protein - aqua
18	67	18.8	447	2	T12544	hypothetical prote
19	64.5	18.1	587	2	JC1419	FC gamma (Igc) rec
20	64.5	18.1	1713	2	A55347	adhesive ligand ep
21	63.5	17.8	180	2	D84092	hypothetical prote
22	63.5	17.8	1810	2	A46227	voltage-dependent
23	63.5	17.8	2193	2	J08564	voltage-dependent
24	63.5	17.8	2193	2	J08564	calcium channel al
25	63.5	17.8	2191	2	A38198	conserved hypothe
26	63.5	17.8	2203	2	T42742	voltage-dependent
27	63	17.6	316	2	C82085	acetyl-CoA C-acety
28	61.5	17.2	392	2	T45290	probable large ATP
29	60.5	16.9	840	2	T36175	

YNT20 protein - ye
Cl protein - tobac
phytoene synthase
zinc finger protein
zinc finger protein
probable peptidyl-
gamma-aminobutylat
hypothetical prote
hypothetical prote
30S ribosomal prot
acetyl-ornithine d
hypothetical prote
hypothetical prote
mycelial surface a
hypothetical prote
probable retroloam

30 60 16.8 269 2 S61633
31 60 16.8 295 2 D42452
32 60 16.8 352 2 S45621
33 60 16.8 352 2 S45621
34 60 16.8 1888 2 T14273
35 59.5 16.7 299 2 B71967
36 59.5 16.7 470 2 T46814
37 59.5 16.7 2137 2 T05244
38 59.5 16.7 4385 2 T29042
39 58.5 16.4 127 2 E96883
40 58.5 16.4 377 2 T52067
41 58.5 16.4 706 2 B71967
42 58.5 16.4 706 2 B71967
43 58.5 16.4 1203 2 T17415
44 58.5 16.4 1232 2 S40766
45 58.5 16.4 1501 2 C84512

ALIGNMENTS

RESULT 1
QOCVLI
AlI protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1995 #sequence-revision 28-Aug-1995 #text-change 08-Apr-1994
B:Hamilton, W.D.O.; Stein, V.E.; Coutlis, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AlI protein

Query Match 95.2% Score 340: DB 1: Length 352:
Query Seq. Similarity 95.2%; P: 340: 46:31; 3: Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 0;

Oy 1 TLVNGEFQVDSARGGCGTSDNAAEALNASSKEEALQIIIRKIPKLYLFAALNSNL 60
|||||
DB 111 TLVNGEFQVDSARGGCGTSDNAAEALNASSKEEALQIIIRKIPKLYLFAALNSNL 170
|||||
Oy 61 DRIFDKTPPEP 70
DB 171 DRIFDKTPPEP 180

RESULT 2
QOCVPT
AlI protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 16-Jun-2000
C:Accession: J00364
B:Coutlis, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; MUID:91311403
A:Accession: J00364
A:Status: translation not shown
A:Residues: 1-361 <COU>
A:Cross-references: GB:D00940; NID:g222458; PTID:BA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AlI protein

DB 110 TLNCFQIDGSRAGCQSNDAAYQAALNTGCKSEALNVILAPKDYVLOFHNLNSUL 169

QY 61 DRI-----FDKTPPE 69
 |||
DB 170 DRIFTFPLEVIVSGPFLSSSFRDYPE 194

RESULT 5
S39211
gene G1 protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S39211
R:Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL data library, August 1993
A:Reference number: S39209
A:Accession: S39211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <NON>
A:Cross-references: EMBL:225751; NID:g433655; PID:CA81026.1; PID:g433658
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 60.4%; Score 217; DB 2; Length 359;
Best Local Similarity 59.4%; Pred. No. 4, 3e-17;
Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 2 LNWGFQVGVRARGCGTSDNDAAEALNASSKEEAQTIREKIPEKYLFAPAALNSULD 61
 |||||
DB 111 LNWGTFQIGSRAGCQSQGTANDTAANINAGSKSLDWIKELAPRDYLHFNHINSULD 170

QY 62 RIFDKTPPE 70
 |||
DB 171 RVFQVPAP 179

RESULT 6
JQ2327
ALL protein - Indian cassava mosaic virus
N:Alternate names: replication-associated protein
C:Species: Indian cassava mosaic virus
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
C:Accession: JQ2327; S35483
R:Hong, C.; Robinson, P.; Harrison, B.D.
A:Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-t
A:Reference number: JQ2326; MUID:94065670
A:Accession: JQ2327
A:Molecule type: DNA
A:Residues: 1-351 <NON>
A:Cross-references: EMBL:224758; NID:g395351; PID:CA80891.1; PID:g584046
C:Superfamily: tomato golden mosaic virus ALL protein

Query Match 59.4%; Score 212; DB 2; Length 351;
Best Local Similarity 62.7%; Pred. No. 1, 5e-16;
Matches 42; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 4 WGEFOVGRSARGCGTSDNFDAAEALNASSKEEAQTIREKIPEKYLFAPAALNSLDRI 63
 |||||
DB 113 WGEFOVGRSARGCGQSANDTAANINAGSKSLDWIKELAPRDYLHFNHINSULD 172

QY 64 FDKTPPE 70
 |||
DB 173 FRKPEPP 179

RESULT 7
S39211
hypothetical protein C4 - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus

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GenCore version 4.5
Copyright (c) 1995 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:37 ; Search time 144.17 Seconds
(without alignments)
35.965 Million cell updates/sec

Title: US-09-289-346a-7

Perfect score: 359

Sequence: 1 TLMGCFQVDSRGSGCQT.....FOFHNLNSALAAIFDKTPEP 70

Scoring table:

BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74072300 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A: Geneseq 1101: *
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT: *
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT: *
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT: *
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT: *
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT: *
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT: *
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT: *
8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT: *
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT: *
10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT: *
11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT: *
12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT: *
13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT: *
14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT: *
15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT: *
16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT: *
17: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT: *
18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT: *
19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT: *
20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT: *
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT: *
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	70	21 AAB18683	Mutant peptide der
2	342	95.3	70	21 AAB18677	Peptide fragment f
3	342	95.3	356	21 AAB18687	Amino acid sequenc
4	334	93.0	70	21 AAB18685	Mutant peptide der
5	330	91.9	70	21 AAB18693	Mutant peptide der
6	328	91.4	70	21 AAB18684	Mutant peptide der
7	328	91.4	70	21 AAB18690	Mutant peptide der
8	328	91.4	70	21 AAB18690	Mutant peptide der
9	327	91.1	70	21 AAB18678	Mutant peptide der
10	327	91.1	70	21 AAB18686	Mutant peptide der
11	326	90.8	70	21 AAB18689	Mutant peptide der

12	324	90.3	70	21 AAB18680	Mutant peptide der
13	324	90.3	70	21 AAB18691	Mutant peptide der
14	321	89.4	70	21 AAB18681	Mutant peptide der
15	316	87.2	70	21 AAB18682	Mutant peptide der
16	310	86.4	70	21 AAB18676	Mutant peptide der
17	213	59.3	353	18 AAM34338	Bean golden mosaic
18	213	59.3	353	18 AAM34332	Bean golden mosaic
19	213	59.3	353	18 AAM34333	Bean golden mosaic
20	213	59.3	353	18 AAM34335	Bean golden mosaic
21	213	59.3	353	18 AAM34335	Bean golden mosaic
22	211	58.8	353	17 AAP70400	ORF 4 gene product
23	211	58.8	353	17 AAP70400	ORF 4 gene product
24	211	58.8	359	17 AAR88871	Sardinian tomato y
25	211	58.8	359	17 AAR88872	Sardinian tomato y
26	211	58.8	361	18 AAM34336	Tomato mottle viru
27	211	58.8	361	18 AAM34324	Tomato mottle viru
28	211	58.8	361	18 AAM34325	Tomato mottle viru
29	211	58.8	361	18 AAM34326	Tomato mottle viru
30	206.5	58.1	361	19 AAY96595	Product of ORF 4
31	193	53.8	357	18 AAM34331	Tomato yellow leaf
32	193	53.8	357	18 AAM34329	Tomato yellow leaf
33	193	53.8	357	18 AAM34330	Tomato yellow leaf
34	193	53.8	357	18 AAM34331	Tomato yellow leaf
35	185	51.5	357	18 AAM34337	Tomato yellow leaf
36	68	18.9	447	21 AAY96595	Human secreted pro
37	68	18.9	447	21 AAY87089	Human secreted pro
38	68	18.9	447	21 AAY65744	Membrane-bound pro
39	68	18.9	447	21 AAY87089	Human secreted pro
40	68	18.9	447	22 AAB05267	Human adult aorta
41	68	18.9	447	22 AAB05267	Human adult aorta
42	68	18.9	447	22 AAB05267	Human adult aorta
43	68	18.9	456	21 AAY87190	Human secreted pro
44	68	18.9	456	22 AAR06167	Human gene 26 enco
45	63.5	17.7	619	13 AAR27651	Human calcium chan
46	63.5	17.7	2161	14 AAR33545	Sequence of the al

ALIGNMENTS

RESULT	1
AA18683	AA18683 standard; peptide; 70 AA.
ID	AA18683 standard; peptide; 70 AA.
AC	AA18683
XX	AA18683
DT	22-JAN-2001 (first entry)
DE	Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
DE	Geminivirus; replication protein; Rep protein; A11; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.
XX	Synthetic.
OS	Tomato golden mosaic virus.
XX	Tomato golden mosaic virus.
XX	Key Location/Qualifiers
FT	Misc-difference 59
FT	Misc-difference 61 /note= "wild type residue replaced with Ala"
FT	Misc-difference 62 /note= "wild type residue replaced with Ala"
FT	Misc-difference 62 /note= "wild type residue replaced with Ala"
XX	W0200054573-A1.
XX	21-SEP-2000.
XX	15-MAR-2000; 2000MO-US06759.
XX	18-MAR-1999; 99US-0125004.
PR	09-APR-1999; 99US-0289346.
XX	(UYNC-) UNIV NORTH CAROLINA STATE.

comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant Ail1 protein with a mutation in the 6b binding region

Claim 53: Page 46, 73pp: English.

The present sequence represents a mutant peptide, derived from a geminivirus replication (rep) protein, also known as Ail1, which binds to the 6b protein of the geminivirus DNA, also known as Ail2, to form a DNA and Ail1 complex with other viral and host proteins. Mutants of the Ail1 protein are used to produce transgenic plants. The mutation in Ail1 is present in a ribosome binding region, and expression of mutant Ail1 protein imparts increased resistance to geminivirus infection in the plant. Mutant Ail1 proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl virus, African cassava mosaic virus, Indian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA:

Query Match	93.0%	Score	334.	DB 21:	Length	70;			
Best Local Similarity	94.3%	Pred. No.	8.4e-36;						
Matches	66;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
QV	1	TLWGVEFQVDRSGAGCGCTSDAAAEALNASKEEAQLIIREKTPKTYLQFHNINSAL	60						
DB	1	tlwgvefqvdrsgagcgctsdaaaealnaskeeaqlirektpktylfqfhlnsnl	60						
QV	61	AAIFKTPREP	70						
DB	61	drifaktrep	70						
RESULT	5								
ID	AA818688	standard; peptide; 70 AA.							
XX	AA818688;								
XX	22-JUN-2001	(first entry)							
DE	Mutant peptide derived from amino acids 110-179 of Rep (ALI) protein.								
XX	Geminivirus; replication protein; Rep protein; ALI; transgenic plant;								
XX	ribosome binding region; resistance; geminivirus infection.								
OS	Synthetic.								
XX	Tomato golden mosaic virus.								
XX	Key	Location/Qualifiers							
PH	Misc-difference 19								
FT	/note= "wild type residue replaced with Ala"								
FT	Misc-difference 20								
FT	/note= "wild type residue replaced with Ala"								
XX	W0200054573-AL.								
PW	21-SEP-2000.								
XX	15-MAR-2000; 2000MO-US06759.								
PF	18-MAR-1999; 99US-0125004.								
PR	09-APR-1999; 99US-0289346.								
XX	(UYNC-) UNIV NORTH CAROLINA STATE.								
PA	Hanley-Bowdoin L, Orozco BM, Kong L;								
XX	WPI: 2000-618851/59								
DB									

XX
DR WPT: 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant A11 protein with a mutation in the Rb binding region
PT
PS
XX Disclosure: Page 48; 73pp; English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as A11. A11 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the A11
CC protein are used to produce transgenic plants. The mutation in A11 is
CC present in a ribosome binding region, and expression of mutant A11
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant A11 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA: -
SQ

Query Match 92.2%; Score 331; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.8e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRGARGCGCTSDAAAEALNASKEEAQLIIRKIPKYLQFHNINSL 60
DB 1 tlvwgefqdgrrsrgcgctsdaaaealnaskeeaqlirkeipkylqfhninsl 60
QY 61 AATFDKTPPEP 70
DB 61 drifdatpep 70

RESULT 6
AAB18692
XX ID AAB18692 standard; peptide; 70 AA.
XX AC AAB18692;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX KW Geminivirus; replication protein; Rep protein: A11; transgenic plant;
XX RN ribosome binding region; resistance: geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FH Misc-difference 66 /note- "wild type residue replaced with Ala"
XX FT Misc-difference 69 /note- "wild type residue replaced with Ala"
XX FT /note- "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000: 2000WO-US06759.
XX PR 18-MAR-1999: 99US-0125004.
XX PR 09-APR-1999: 99US-0289346.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI: 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the Rb binding region
XX
XX Disclosure: Page 50; 73pp; English.
XX
PS The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as A11. A11 binds
CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC DNA, and interacts with other viral and host proteins. Mutants of the A11
CC protein are used to produce transgenic plants. The mutation in A11 is
CC present in a ribosome binding region, and expression of mutant A11
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant A11 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA:
SQ

Query Match 91.9%; Score 330; DB 21; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.8e-35;
Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGEFQDGRGARGCGCTSDAAAEALNASKEEAQLIIRKIPKYLQFHNINSL 60
DB 1 tlvwgefqdgrrsrgcgctsdaaaealnaskeeaqlirkeipkylqfhninsl 60
QY 61 AATFDKTPPEP 70
DB 61 drifdatpep 70

RESULT 7
AAB18684
XX ID AAB18684 standard; peptide; 70 AA.
XX AC AAB18684;
XX DT 22-JAN-2001 (first entry)
XX DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX KW Geminivirus; replication protein; Rep protein: A11; transgenic plant;
XX RN ribosome binding region; resistance: geminivirus infection.
XX OS Synthetic.
XX OS Tomato golden mosaic virus.
XX FH Key Location/Qualifiers
XX FH Misc-difference 7 /note- "wild type residue replaced with Ala"
XX FT Misc-difference /note- "wild type residue replaced with Ala"
XX PN WO200054573-A1.
XX PD 21-SEP-2000.
XX PF 15-MAR-2000: 2000WO-US06759.
XX PR 18-MAR-1999: 99US-0125004.
XX PR 09-APR-1999: 99US-0289346.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PI

XX Hanley-Bowdoin L, Orozco BW, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT
 XX Claim 52; Page 45; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC transgenic plants. A11 proteins are useful for producing plants having as
 CC increased resistance to geminivirus infection as the wild type A11 protein.
 CC The present sequence represents a mutant peptide, derived from the
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;

Query Match 91.4%; Score 328; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 5e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0;

QY 1 TLVWGFQVQDSRGCGCOTSDNDAALNASSKEFALQIIRKIPKYLQFHNLSAL 60

Db 1 TLVWGFQVQDSRGCGCOTSDNDAALNASSKEFALQIIRKIPKYLQFHNLSAL 60

QY 61 AAIFDKTPEP 70

Db 61 dfrfdktpep 70

RESULT 8
 AAB18690
 ID AAB18690 standard; peptide; 70 AA.

XX AAB18690;
 XX 22-JAN-2001 (first entry)
 XX
 DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.
 XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
 XX
 FT Misc-difference 27 /note= "wild type residue replaced with Ala"
 FT Misc-difference 30 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-US06759.

XX 18-MAR-1999; 99US-0125004.

XX 09-APR-1999; 99US-0289346.

XX (UNY-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BW, Kong L;
 XX WPI; 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 PT
 XX Disclosure; Page 49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC transgenic plants. A11 proteins are useful for producing plants having as
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA;

Query Match 91.4%; Score 328; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 5e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVWGFQVQDSRGCGCOTSDNDAALNASSKEFALQIIRKIPKYLQFHNLSAL 60

Db 1 TLVWGFQVQDSRGCGCOTSDNDAALNASSKEFALQIIRKIPKYLQFHNLSAL 60

QY 61 AAIFDKTPEP 70

Db 61 dfrfdktpep 70

RESULT 9
 AAB18678
 ID AAB18678 standard; peptide; 70 AA.

XX AAB18678;
 XX 22-JAN-2001 (first entry)
 XX

DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX
 KW Geminivirus; replication protein; Rep protein; A11; transgenic plant;
 KW ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
 XX
 FT Misc-difference 12 /note= "wild type residue replaced with Ala"
 FT Misc-difference 13 /note= "wild type residue replaced with Ala"

XX WO2000054573-A1.

XX 21-SEP-2000.

```

FF 15-MAR-2000: 2000WO-US06759.
XX
XX 18-MAR-1999: 99US-0125004.
XX
XX 09-APR-1999: 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the Rb binding region
XX
XX
XX Claim 53: Page 42-43: 73pp: English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as A11. A11 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the A11
XX protein are used to produce transgenic plants. The mutation in A11 is
XX present in a ribosome binding region, and expression of mutant A11
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant A11 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, cotton leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:
XX
XX
XX Query Match 91.18: Score 327; DB 21: Length 70;
XX Best Local Similarity 91.44: Pred. No. 6.8e-35;
XX Matches 64: Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 TLVGEFVQDGRSGCGCTSDNDAAEALNASSKEALQIREKIPKYLQFHNLSAL 60
XX Db 1 tlvgwefvqdaaaggcctsdndaeealnasskealqirekipekylqfhnlsnl 60
XX
XX QY 61 AAIFDKTPEP 70
XX Db 61 drifdktpetp 70
XX
XX
XX RESULT 10
XX AAB18686
XX ID AAB18686 standard; peptide: 70 AA.
XX
XX AC AAB18686;
XX
XX XX 22-JAN-2001 (first entry)
XX
XX XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX
XX XX Geminivirus: replication protein; Rep protein; A11; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX XX Synthetic.
XX
XX XX Tomato golden mosaic virus.
XX
XX XX Key Location/Qualifiers
XX XX Misc-difference 25 /note- "wild type residue replaced with Leu"
XX XX Misc-difference 25 /note- "wild type residue replaced with Leu"
XX XX Misc-difference 26 /note- "wild type residue replaced with Leu"
XX XX Misc-difference 26 /note- "wild type residue replaced with Leu"
XX

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FN W0200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000: 2000WO-US06759.
XX
XX 18-MAR-1999: 99US-0125004.
XX
XX 09-APR-1999: 99US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant A11 protein with a mutation in the Rb binding region
XX
XX
XX Claim 53: Page 46: 73pp: English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as A11. A11 binds
XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the A11
XX protein are used to produce transgenic plants. The mutation in A11 is
XX present in a ribosome binding region, and expression of mutant A11
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant A11 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, cotton leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:
XX
XX
XX Query Match 91.18: Score 327; DB 21: Length 70;
XX Best Local Similarity 91.44: Pred. No. 6.8e-35;
XX Matches 64: Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 TLVGEFVQDGRSGCGCTSDNDAAEALNASSKEALQIREKIPKYLQFHNLSAL 60
XX Db 1 tlvgwefvqdgrrsgcgctsdndllealnasskesalqirekipekylqfhnlsnl 60
XX
XX QY 61 AAIFDKTPEP 70
XX Db 61 drifdktpetp 70
XX
XX
XX RESULT 11
XX AAB18689
XX ID AAB18689 standard; peptide: 70 AA.
XX
XX AC AAB18689;
XX
XX XX 22-JAN-2001 (first entry)
XX
XX XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX
XX XX Geminivirus: replication protein; Rep protein; A11; transgenic plant;
XX ribosome binding region; resistance; geminivirus infection.
XX
XX XX Synthetic.
XX
XX XX Tomato golden mosaic virus.
XX
XX XX Key Location/Qualifiers
XX XX Misc-difference 22 /note- "wild type residue replaced with Ala"
XX XX Misc-difference 23 /note- "wild type residue replaced with Ala"
XX

```

FT XX /note= "wild type residue replaced with Ala"
 FN W0200054573-AL.
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 XX
 XX Disclosure: Page 48-49: 73pp: English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, bean golden mosaic
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 XX
 XX Query Match 90.8%; Score 326; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 9.1e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 TLVWGFEVQGRSARGCCTSDNDAARALNASSKEEALQIIRKIPKYLQFHNLSAL 60
 DB 1 TLVWGFQVGRSARGCCTSDNDAARALNASSKEEALQIIRKIPKYLQFHNLSAL 60
 OY 61 AAIFDKTPEP 70
 DB 61 dfrldktpep 70
 XX
 XX RESULT 12
 XX AAB18680
 XX AAB18680 standard: peptide; 70 AA.
 XX
 XX AC AAB18680;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 DE Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 42
 FT

FT Misc-difference 43
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 44
 FT /note= "wild type residue replaced with Ala"
 FN W0200054573-AL.
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US06759.
 XX
 PR 18-MAR-1999; 99US-0125004.
 PR 09-APR-1999; 99US-0289346.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 PI Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant A11 protein with a mutation in the Rb binding region
 XX
 XX Claim 52; Page 43-44: 73pp: English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11 is
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, bean dwarf mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC cassava mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 XX
 XX Query Match 90.3%; Score 324; DB 21; Length 70;
 Best Local Similarity 91.4%; Pred. No. 1.7e-34;
 Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 TLVWGFEVQGRSARGCCTSDNDAARALNASSKEEALQIIRKIPKYLQFHNLSAL 60
 DB 1 TLVWGFQVGRSARGCCTSDNDAARALNASSKEEALQIIRKIPKYLQFHNLSAL 60
 OY 61 AAIFDKTPEP 70
 DB 61 dfrldktpep 70
 XX
 XX RESULT 13
 XX AAB18691
 XX AAB18691 standard: peptide; 70 AA.
 XX
 XX AC AAB18691;
 XX
 XX 22-JAN-2001 (first entry)
 XX
 XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 DE Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 42
 FT

Job time: 154 sec

DT 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (All) protein.
 DE
 XX Geminivirus; replication protein; Rep protein; All; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 KW
 XX Synthetic.
 OS
 XX Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 PH
 FT Misc-difference 52 /note- "wild type residue replaced with Ala"
 FT Misc-difference 54 /note- "wild type residue replaced with Ala"
 FT Misc-difference 55 /note- "wild type residue replaced with Ala"
 FT Misc-difference 55 /note- "wild type residue replaced with Ala"
 FT
 XX W0200054573-Al.
 PN
 XX 21-SEP-2000.
 DE
 XX 15-MAR-2000; 2000WO-US06759.
 PF
 XX 18-MAR-1999; 99US-0125004.
 PR
 XX 09-APR-1999; 99US-0289346.
 PR
 XX (UFGC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI
 XX WPI: 2000-618851/59.
 DR
 XX
 XX Transgenic plants with increased resistance to geminivirus infection
 XX comprise a nucleic acid construct containing a nucleic acid sequence
 XX encoding a mutant All protein with a mutation in the Rb binding region
 XX .
 XX
 XX Claim 53; Page 44-45; 73pp: English.
 PS
 XX
 XX The present sequence represents a mutant peptide, derived from a
 XX geminivirus replication (Rep) protein, also known as All. All binds
 XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 XX DNA, and interacts with other viral and host proteins. Mutants of the All
 XX protein have been identified that are resistant to geminivirus infection.
 XX present in a ribosome binding region, and expression of mutant All
 XX protein imparts increased resistance to geminivirus infection in the
 XX plant. Mutant All proteins are useful for producing plants having
 XX increased resistance or reduced sensitivity to a geminivirus such as
 XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 XX cassava mosaic virus, Potato yellow mosaic virus, bean golden mosaic
 XX virus, bean golden mosaic virus, bean golden mosaic virus, bean golden
 XX virus, cotton leaf curl virus or beet curly top virus.

Sequence 70 AA:

Query Match 88.6%; Score 318; DB 21; Length 70;
 Local similarity 91.4%; Positives 36; Gaps 0;
 Matches 64; Conservative 0; Mismatches 6; Indels 0;

Oy 1 TLVWGEFQVDRSARGCQTSNDAAEALNASSKEEALQITREIPEKYLQFPHINSAL 60
 |||||
 Db 1 tlwgefvdgrsargcqtndaaaealnasskeaalqilrekipekylfaalnsl 60
 |||||
 Oy 61 AAIFDTPPEP 70
 |||||
 Db 61 drlfttpep 70

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